1/89

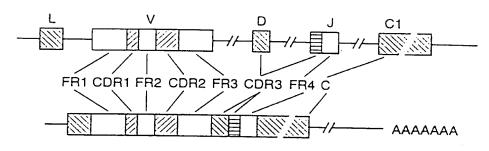


FIG. 1

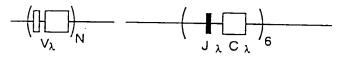


FIG. 2

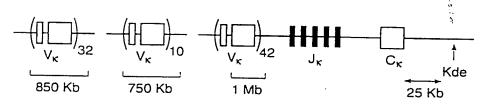
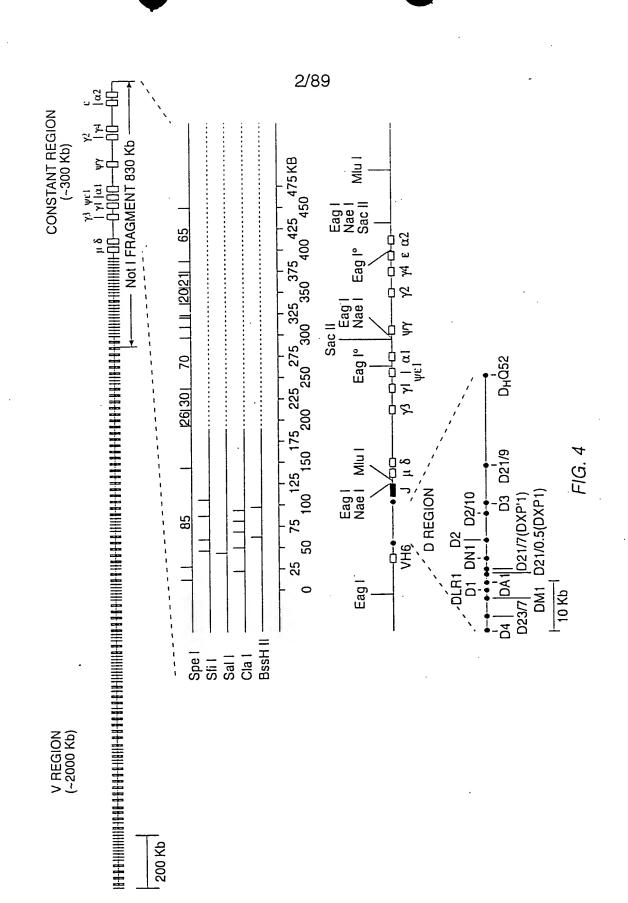


FIG. 3





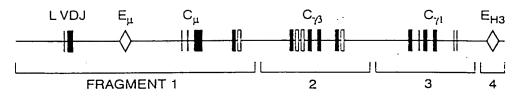


FIG. 5

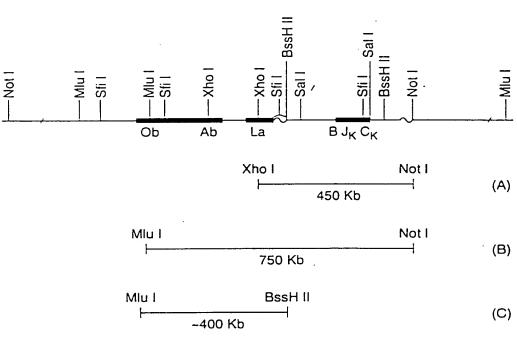
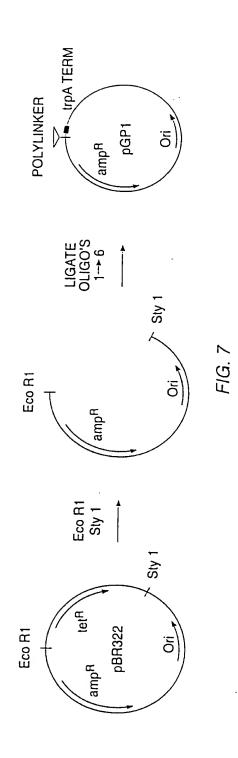


FIG. 6

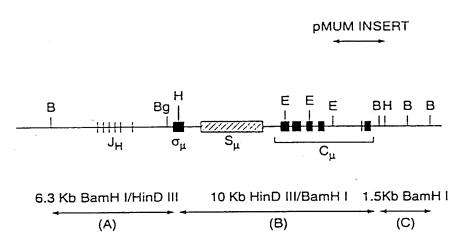




OLIGO-1		OLIGO-3
OLIGO-4	OLIGO-5	OLIGO-6
	56 BamH I 89 Xh 42 Sfi I 75 Cla I 40 Not I 65 BssH II	115 Kpn I 111 Sma I Sph I 127 Mlu I Io I 121 HinD III 106 EcoR I 139 Not I 100 Bgl II 133 Spe I
147 BASE PAIRS		

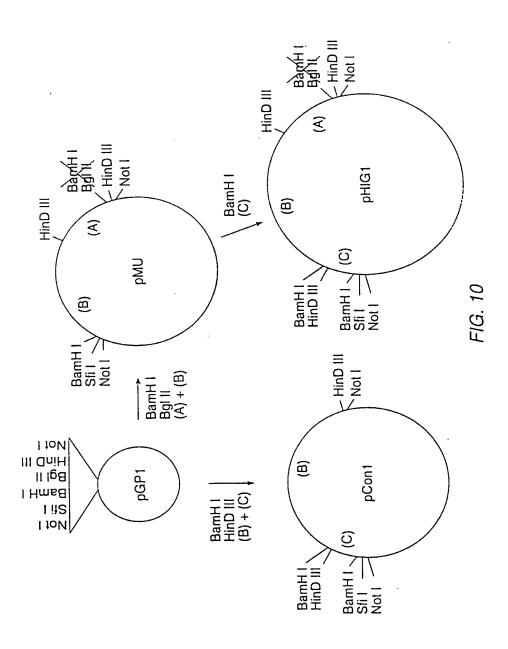
FIG. 8

pGP1 POLYLINKER

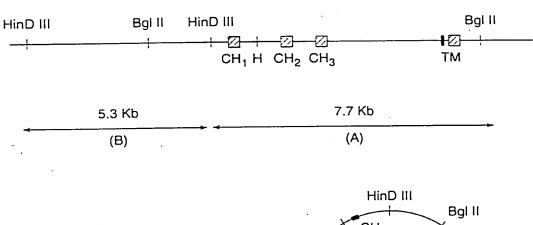


HUMAN μ LOCUS

FIG. 9



HUMAN $C_{\gamma l}$ GENE



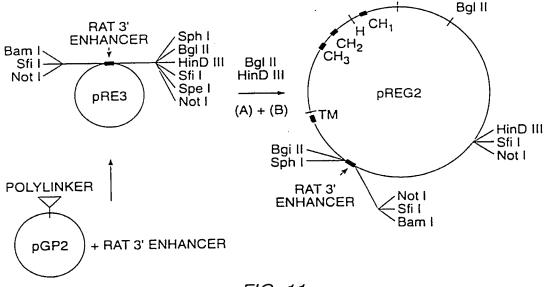
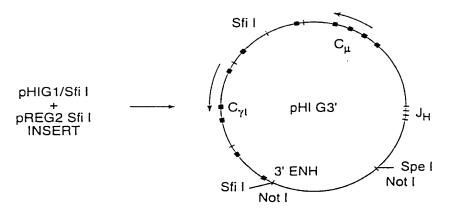
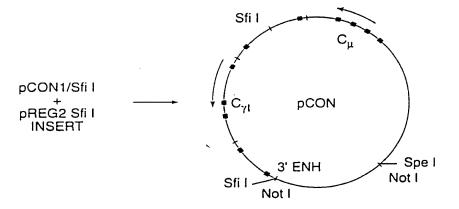


FIG. 11



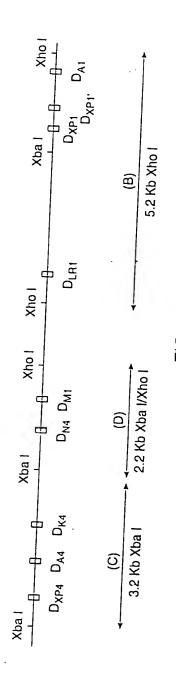
31.5 Kb Not I/Spe I INSERT

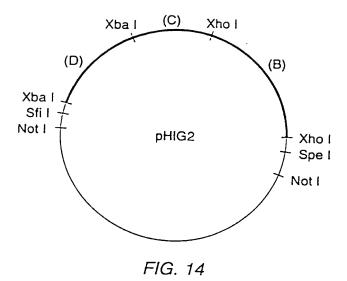


25 Kb Not I/Spe I INSERT

FIG. 12

HUMAN D REGION







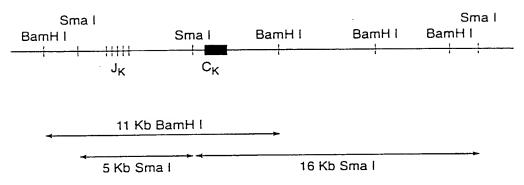


FIG. 15

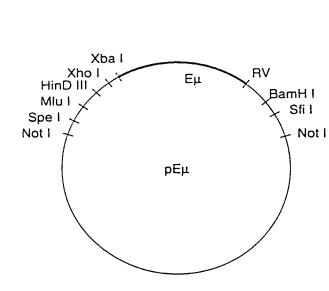
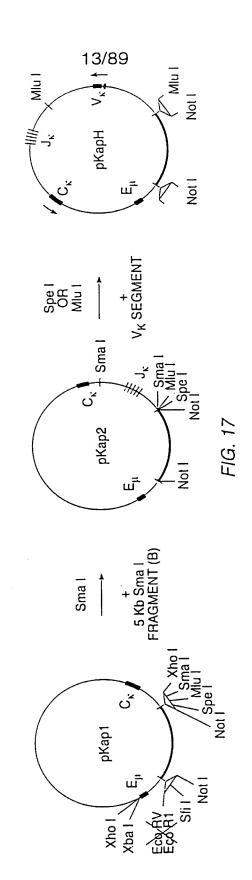


FIG. 16



MOUSE HEAVY CHAIN LOCUS

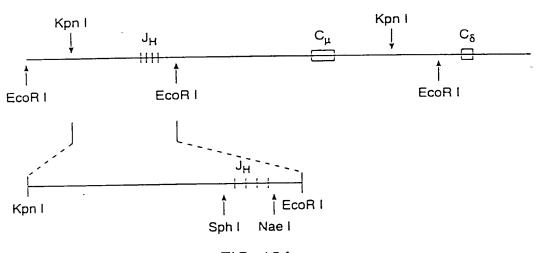


FIG. 18A



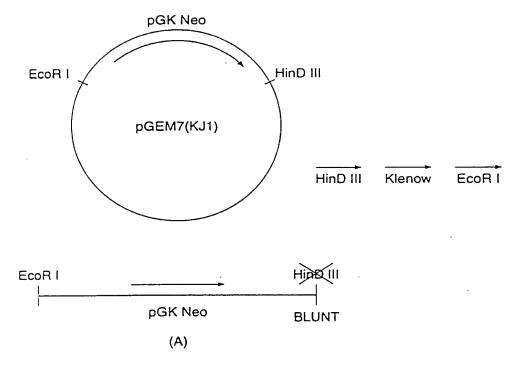
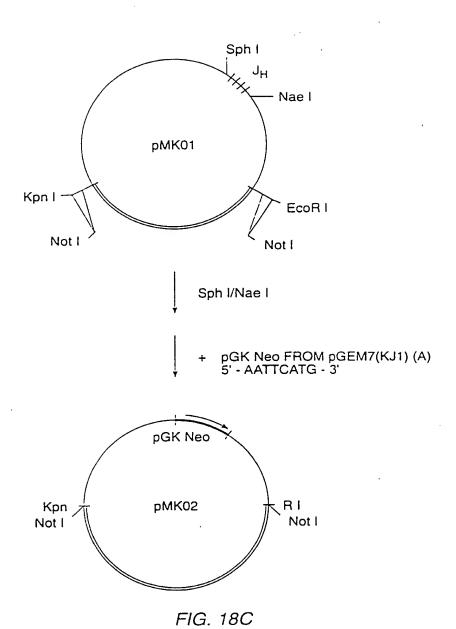
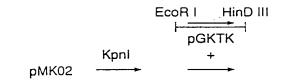


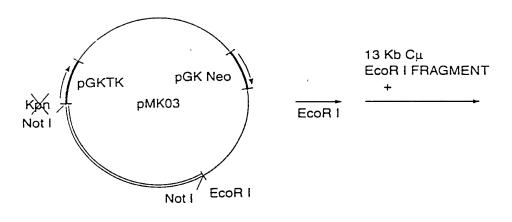
FIG. 18B

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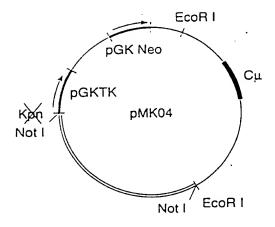


FIG. 18D



MOUSE KAPPA GENE

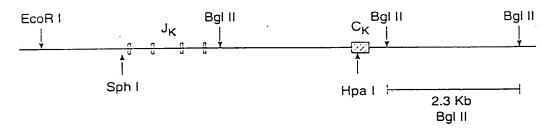


FIG. 19A



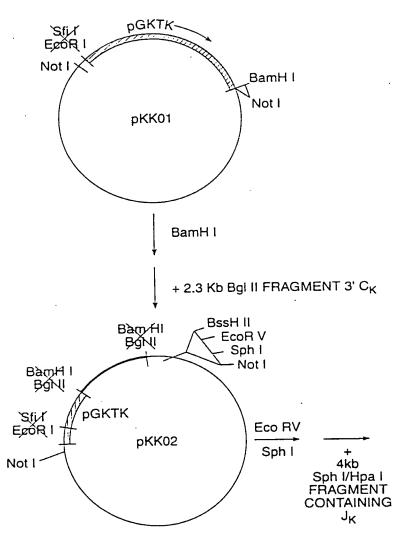
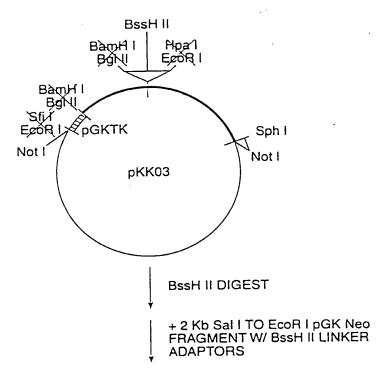


FIG. 19B





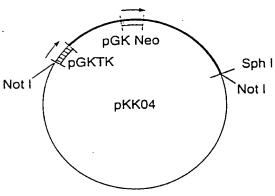
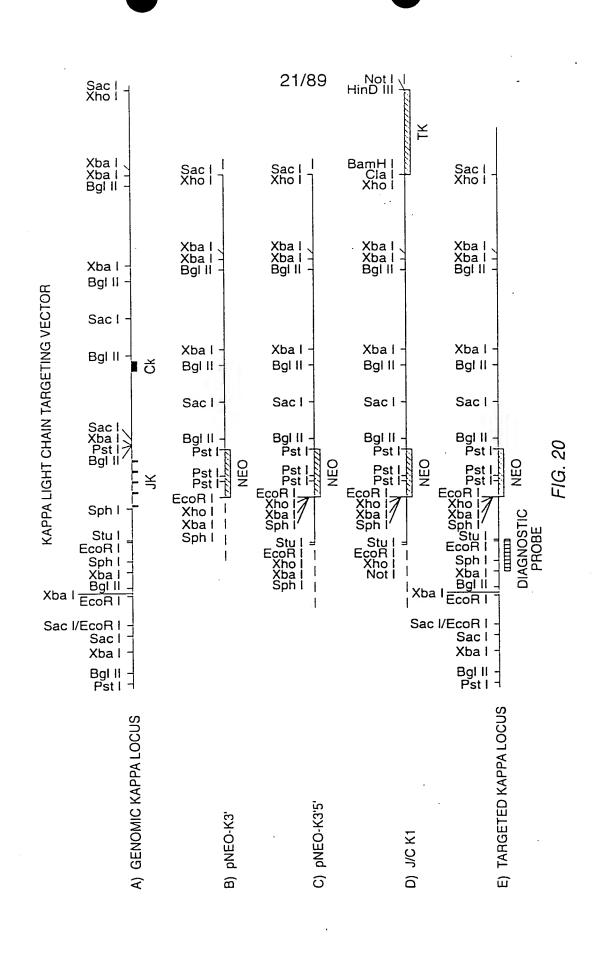
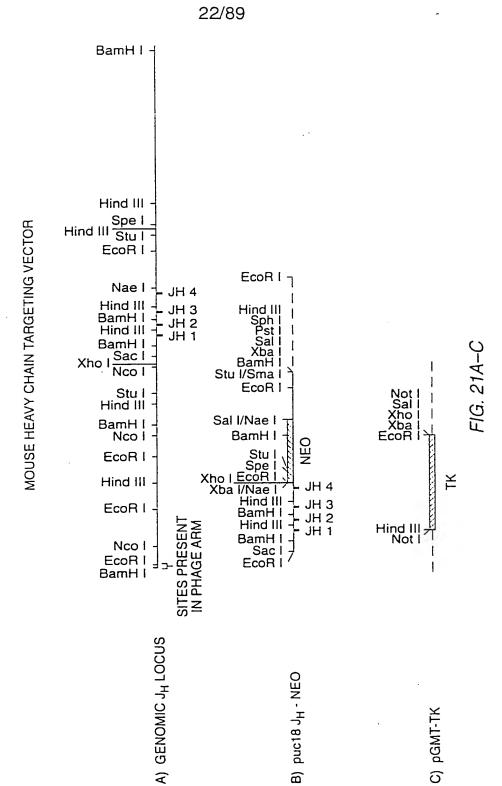


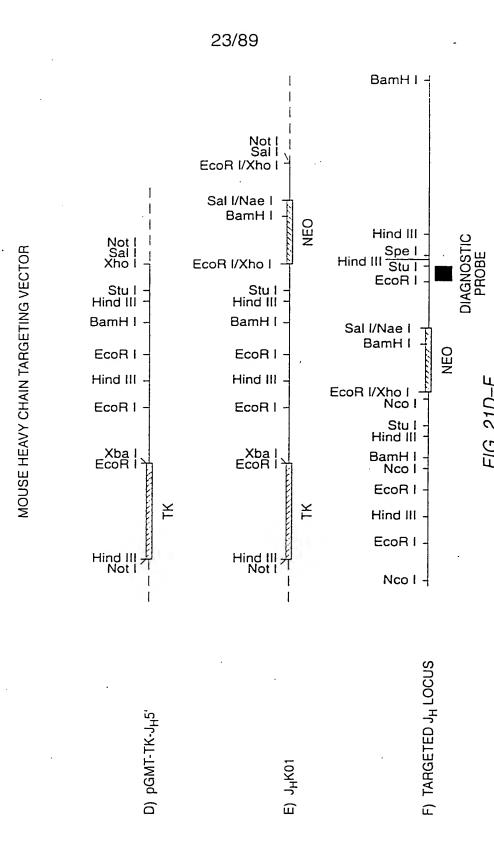
FIG. 19C













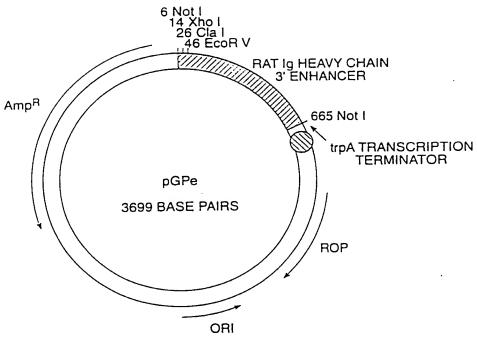
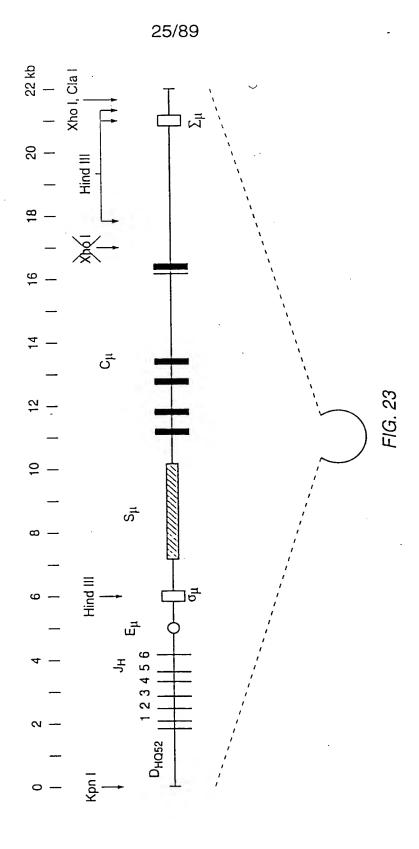
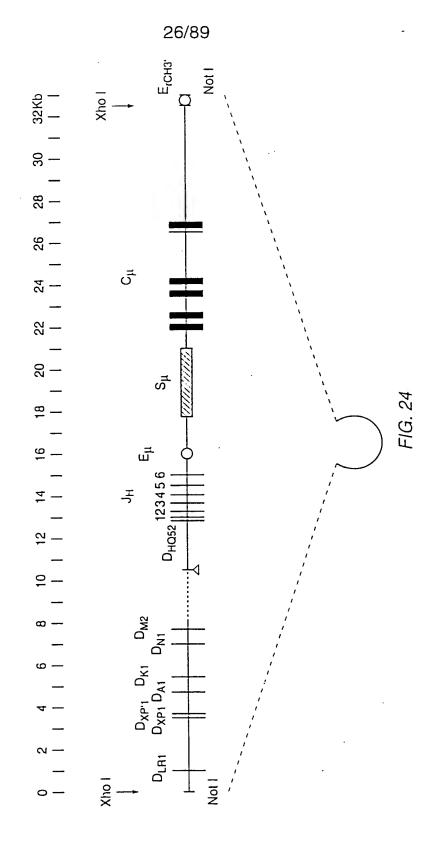
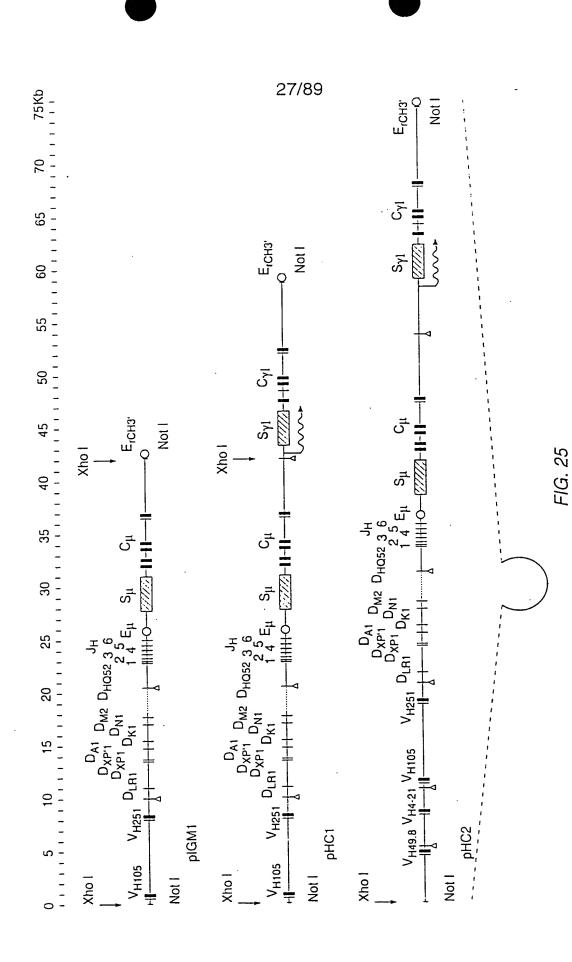
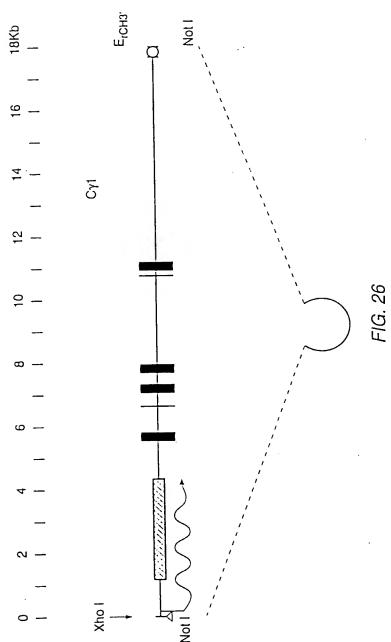


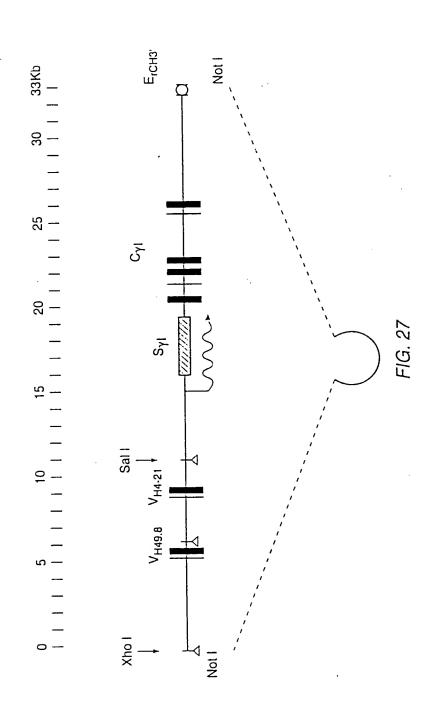
FIG. 22

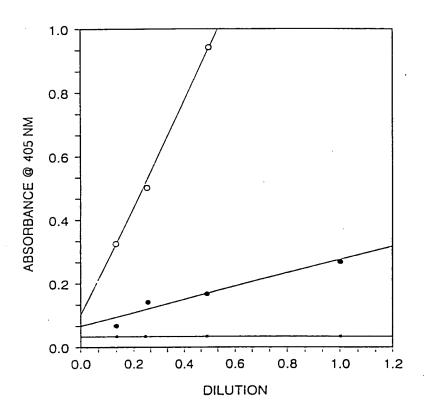








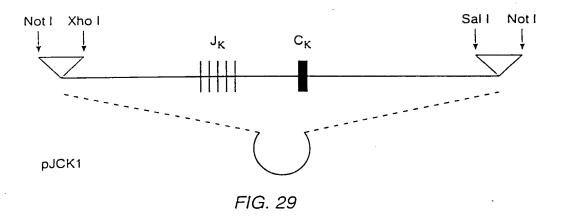


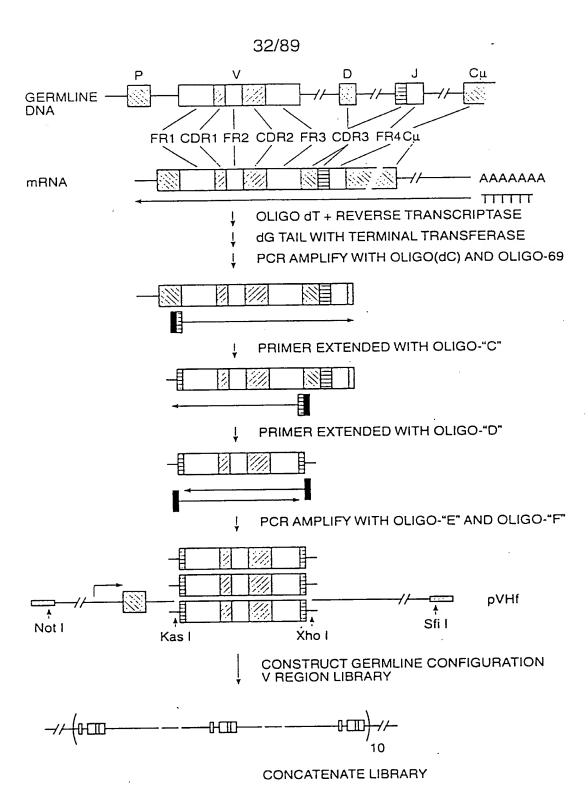


o IgM pHC1 TRANSGENIC
• IgG1 PHC1 TRANSGENIC

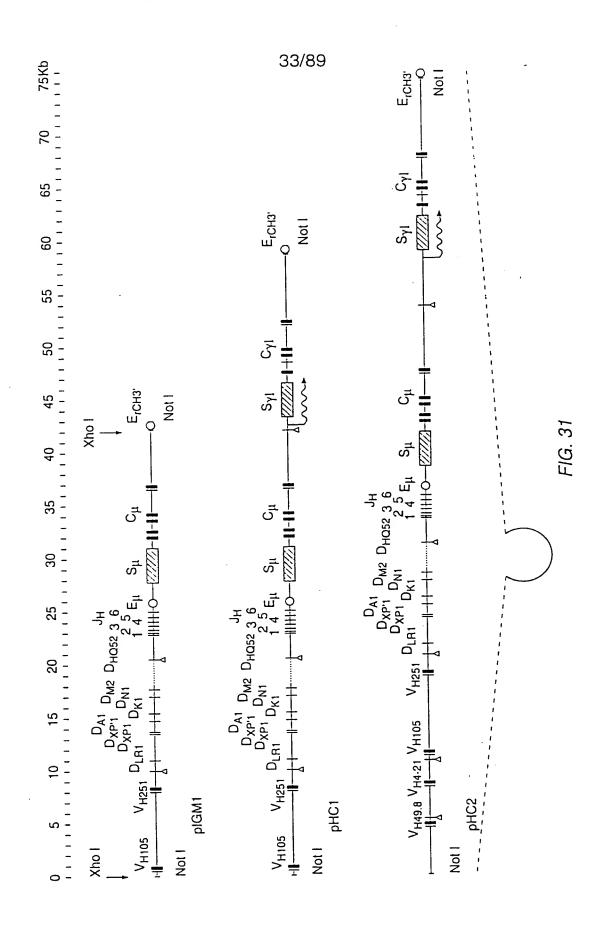
* IgM NON-TRANSGENIC CONTROL

FIG. 28

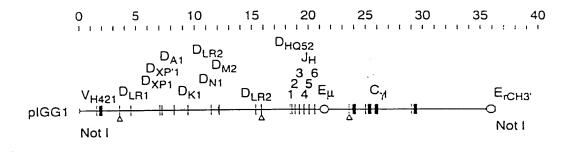


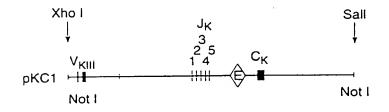


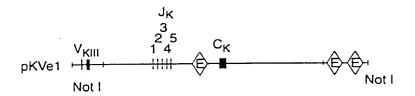
SYNTHETIC HEAVY CHAIN VARIABLE REGION FIG. 30











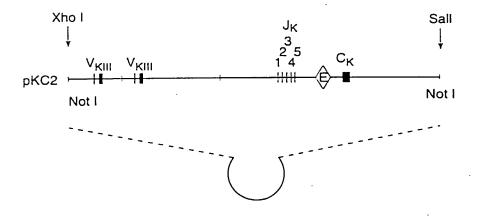
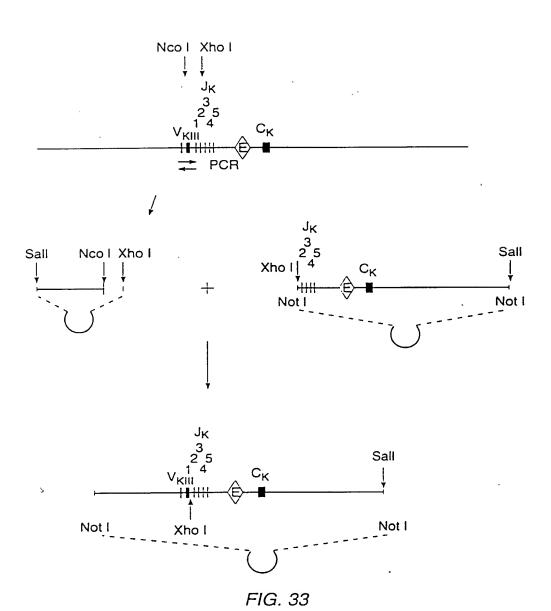
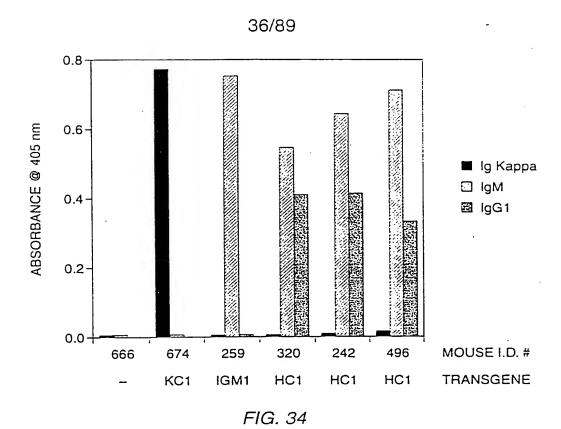
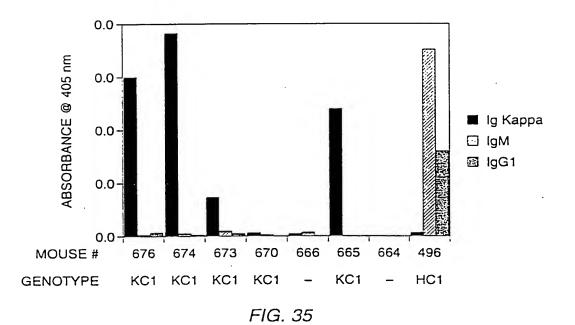
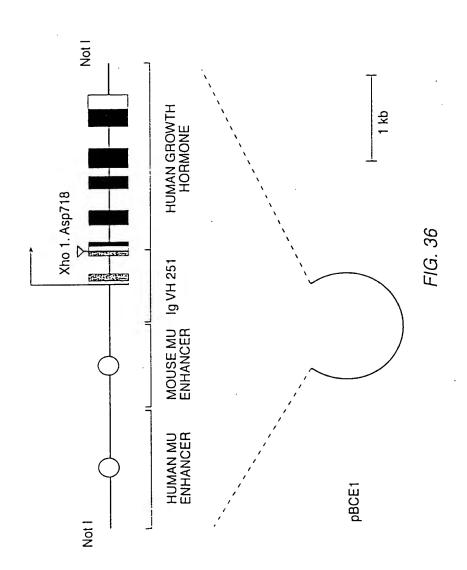


FIG. 32









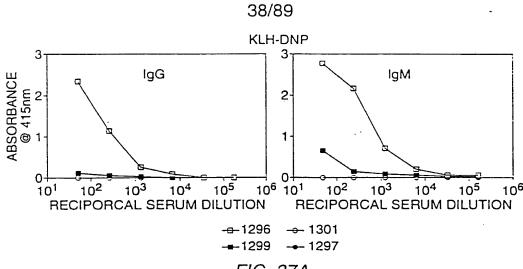
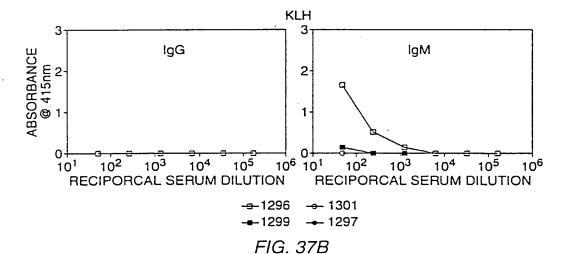
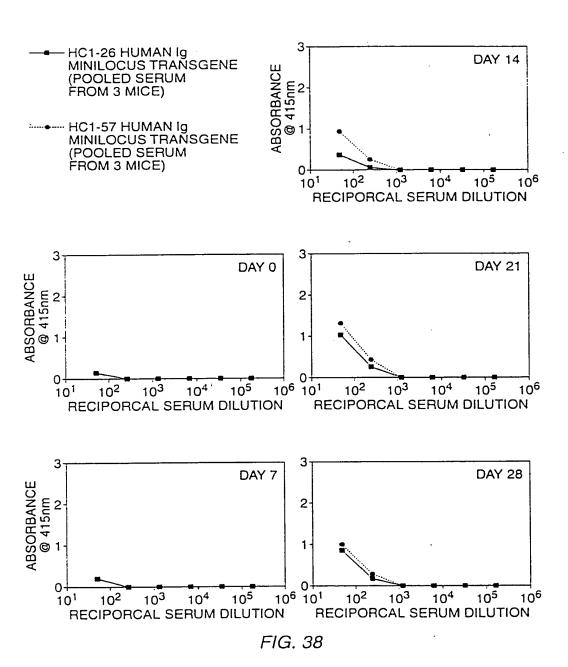


FIG. 37A



BSA-DNP ABSORBANCE @ 415nm L N lgG lgM 2 1 --| 0+-10° 10¹ 10² 103 10⁴ 10⁵ 10³ 10⁴ 10¹ RECIPORCAL SERUM DILUTION RECIPORCAL SERUM DILUTION -a-1296 - 1301 --1299 --- 1297

FIG. 37C





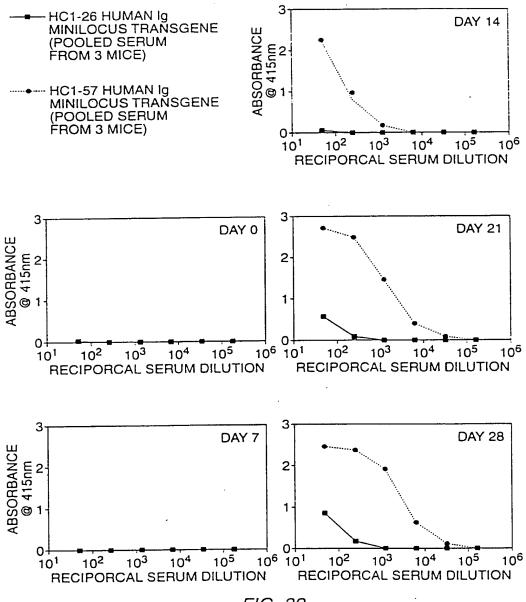


FIG. 39

101102108 	CCTTTGATCATG	mACM-MACMACC	CTACCC			:	AACTGGTTCGACCCCCTG	tattat PACTACTACTACGCTATGGACGTCACG	E	
KID.	CAGGGGGGGATA	CATTGGctaaAtggggaT CGGattacgatattttgactggttattatGCG	GGgtattaTtatgAttcggggaCttattataaGTCTACCT. ctaactggCTAT.	CAAGG CATCTT CAAACT	CATggtatagcagcagctggtacgtggttcGACCC CAGGGC CATCTT	GCCgggtataCcagcagctggtT CATCTT	GtggttcggggaTttattatT CAAAGGG GGATCGTGG	CTCCCCAATGACAGT CGGGGtactatggttcggggagttattat TACTACTACT	CATGagcagctggtacAGGGT GATATGGGGGGGGCCTC CC	CDR 111
87 88 89 91 94 		661.			===	90	Gtggttcgg			
64 68 71 73 75 76 79 80 8182a82b 83 84 87 88 89 91 94 AAACCGCCAAGATCAGCTACCTGCAGAGGCAAGGCCACCACCATGTAGAGA	9	9	.GTTATAC.GT						A P	
73 75 76 79 80 AAGATCAGCTACCTG			.A. T.	e	. G				Α	
- J	:	: :	_: :	:::::					. J	
	6								J	11
23 24 28 29 30 31 32 35 40 52 56 60 62 64 68 71 AAGGGTAGCTTTACCAGCTACGCCATCTATGATAGCTCCCAAACCGCC				. T. G. A.			32	.a	18	11 000 1

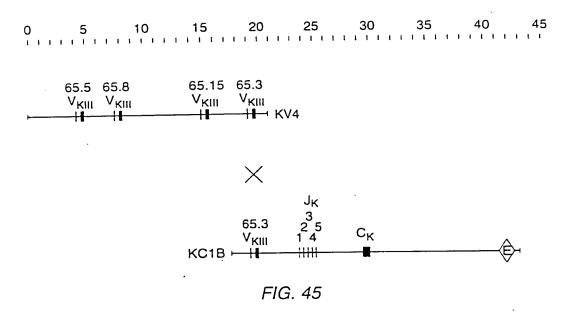
FIG. 40

٦	TTTCTGGCC	TGACAACCAG	GGTGGCGCAG	GATGCTCAGT	GCAGAGAGGA	50
1	AGAAGCAGGT	GGTCTCTGCA	GCTGGAAGCT	CAGCTCCCAC	CCAGCTGCTT	100
-	rgcatgtccc	TCCCAGCTGC	CCTACCTTCC	AGAGCCCATA	TCAATGCCTG	150
-	TGTCAGAGCC	CTGGGGAGGA	ACTGCTCAGT	TAGGACCCAG	AGGGAACCAT Me	200
	GGAAGCCCCA	GCTCAGCTTC	тсттсстсст	GCTACTCTGG		250
	+CluAlaDro	AlaGlnLeuL	euPhel eul e	ul eul euTrp	LeuPro	
•	agggggaacc	atgaggtggt	tttgcacatt	agtgaaaact	cttgccacct	300
		agaaatataa				350
	ctctactcaa	agacagttgg	tttgatcttg	attacatgag	tgcatttctg	400
	tttattcc	aatttcagAT	ACCACCGGAG	AAATTGTGTT	GACACAGTCT	450
		Asp	ThrThrGlyG	luIleValLe	uThrGlnSer	
	CCAGCCACCC	TGTCTTTGTC	TCCAGGGGAA	AGAGCCACCC	TCTCCTGCAG	500
	ProAlaThri	euSerLeuSe	rProGlvGlu	AraAlaThrL	euSerCysAr	
	CCCCACTCAG	AGTGTTAGCA	GCTACTTAGC	CTĞGTACCAA	CAGAAACCTG	550
	allacarcia	SerValSerS	erTvrleuAl	aTroTvrGln	GlnLysProG	
	CCCACCCTCC	CAGGCTCCTC	ATCTATGATG	CATCCAACAG	GGCCACTGGC	600
	1Clastapp	. cAdderecte	. TleTvrAsnA	laSerAsnAr	gAlaThrGly	
	ATCCCACCCA	COTTCACTO	CAGTGGGTCT	GGGACAGACT	TCACTCTCAC	650
	TI -D Al -A	Taphasana a	vSarClvSar	GlvThr4snP	heThrLeuTh	
	CATCACCACC	CTACACCCTO	. yseratyser	VCTTTATTAC	TGTCAGCAGC	700
	CATCAGCAGC	. CIAGAGCCIO	1AcaDhoAl	aValTyrTyr	CysGlnGlnA	
	rileSerSer	Leugluproc	CTOATTCCAC	ATGARACAAA	AACCCCAACA	750
			GIGATICCAC	, ATGAMACAAA	AACCCCAACA	, 50
	rgSerAsnTr	pro	- 47747747			800
	AGACCATCAG	, IGILIACIAC	JAHAHAIAC	. CAGCIGCIIC	CTTTACAGAC	300
	AGCTAGTGG	GT GT			,	812

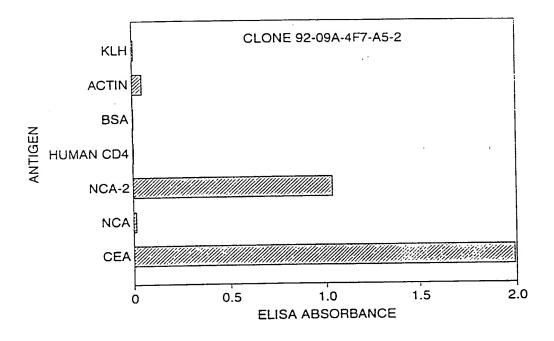
43/89 AGGGCGGCGC AGATGCTCAG TGCAGAGAGA AGAAACAGGT GGTCTCTGCA 50 GCTGGAAGCT CAGCTCCCAC CCCAGCTGCT TTGCATGTCC CTCCCAGCTG 100 CCCTACCTTC CAGAGCCOAT ATCAATGCCT GGGTCAGAGC TCTGGGGAGG 150 AACTGCTCAG TTAGGACCCA GACGGAACCA TGGAAGCCCC AGCGCAGCTT 200 M etGluAlaPr oAlaGlnLeu CTCTTCCTCC TGCTACTCTG GCTCACAGgt gaggggaata tgaggtgtct 250 LeuPheLeuL euLeuLeuTr pLeuThr ttgcacatca gtgaaaactc ctgccacctc tgctcagcaa gaaatataat 300 taaaattcaa aatagatcaa caattttggc tctactcaaa gacagtgggt 350 ttgattttga ttacatgagt gcatttctgt tttatttcca atttcagATA 400 CCACCGGAGA AATTGTGTTG ACACAGTCTC CAGCCACCCT GTCTTTGTCT 450 hrThrGlyGl uIleValLeu ThrGlnSerP roAlaThrLe uSerLeuSer CCAGGGGAAA GAGCCACCCT CTCCTGCAGG GCCAGTCAGG GTGTTAGCAG 500 ProGlyGluA rgAlaThrLe uSerCysArg AlaSerGlnG lyValSerSe CTACTTAGCC TGGTACCAGC AGAAACCTGG CCAGGCTCCC AGGCTCCTCA 550 rTyrLeuAla TrpTyrGlnG lnLysProGl yGlnAlaPro ArgLeuLeuI TCTATGATGC ATCCAACAGG GCCACTGGCA TCCCAGCCAG GTTCAGTGGC 600 leTyrAspAl aSerAsnArg AlaThrGlyI leProAlaAr gPheSerGly AGTGGGCCTG GGACAGACTT CACTCTCACC ATCAGCAGCC TAGAGCCTGA 650 SerGlyProG lyThrAspPh eThrLeuThr IleSerSerL euGluProGl AGATITICA GTITATTACT GTCAGCAGCG TAGCAACTGG CATCCCACAG 700 uAspPheAla ValTyrTyrC ysGlnGlnAr gSerAsnTrp His TGATTCCACA TGANACAAAA ACCCCAACAA GACCATCAGT GTTTACTAGA 750 TTATTATACC AGCTGCTTCC TTTACAGACA GCTAGTGGGG TGGCCACTCA 800 GTGTTAGCAT CTCAGCTCTA TTTGGCCATT TTGGAGTTCA AGTTGTCAAG 850 TCCAAAATTA CTTATGTTAG TCCATTGCAT CATACCATTT CAGTGTGGCT 900

CCGCCCCAGC	TGCTTTGCAT	GTCCCTCCCA	GCCGCCCTGC	AGTCCAGAGC	50
CATATCAAT	GCCTGGGTCA	GAGCTCTGGA	GAAGAGCTGC	TCAGTTAGGA	100
ACCCCAGAGG		AACCCCAGCG uThrProAla			150
ACTCTGGCTC uLeuTrpLeu	CCAGgtgagg	ggaacatggg			200
aaaccctctc	aagtcctgtt	acctggcaac	tctgctcagt	caatacaata	250
attaaagctc	aatataaagc	aataattctg	gctcttctgg	gaagacaatg	300
ggtttgattt	agattacatg	ggtgactttt	ctgttttatt	tccaatctca	350
gATACCACCG	GAGAAATTGT	GTTGACGCAG lLeuThrGln	TCTCCAGGCA	CCCTGTCTTT	400
GTCTCCAGGG	GAAAGAGCCA	CCCTCTCCTG hrLeuSerCy	CAGGGCCAGT	CAGAGTGTTA	450
GCAGCAGCTA	CTTAGCCTGG	TACCAGCAGA TyrGlnGlnL	AACCTGGCCA	GGCTCCCAGG	500
CTCCTCATCT	ATGGTGCATC	CAGCAGGGCC	ACTGGCATCC	CAGACAGGTT	550
CAGTGGCAGT	GGGTCTGGGA	rSerArgAla CAGACTTCAC hrAspPheTh	TCTCACCATC	AGCAGACTGG	600
AGCCTGAAGA	TTTTGCAGTG	TATTACTGTC TyrTyrCysG	AGCAGTATGG	TAGCTCACCT	650
CCCACAGTGA	TTCAGCTTGA	AACAAAAACO	TCTGCAAGAC	CTTCATTGTT	700
TACTAGATTA	TACCAGCTGC	TTCCTTTACA	GATAGCTGCT	GCAATGACAA	750
CTCAATTTAG	CATCTCTCTC	TGCTTGGGCA	TTTTGGGGAT	CTTAAAAAAAG	800
TAATCCCTTG	АТАТАТТТТ	GACTCTGATT	CCTGCATTTT	TCCTCAGACC	850
AAGATGGACA	GCCAGGTTTA	AGCACAGTTT	CACAGTAATG	GCCACTGGAT	900

AAACACATTC ⁻	TCTGCAGACA	AATTTGAGCT	ACCTTGATCT	TACCTGGACA	50
GGTGGGGACA (CTGAGCTGGT	GCTGAGTTAC	TCAGATGCGC	CAGCTCTGCA	100
GCTGTGCCCA (GCCTGCCCCA	TCCCCTGCTC	ATTTGCATGT	TCCCAGAGCA	150
CAACCTCCTG (CCCTGAAGCC	TTATTAATAG	GCTGGTCAGA	CTTTGTGCAG	200
GAATCAGACC	CAGTCAGGAC		CATGAGGGTC pMetArgVal l		250
TCCTGGGGCT euLeuGlyLe		TGTTTCCCAG			300
cagtttactc	agcccagggt	gctcagtact	gctttactat	tcagggaaat	350
tctcttacaa	catgattaat	tgtgtggaca	tttgttttta	tgtttccaat	400
ctcagGTGCC	AGATGTGACA	TCCAGATGAC	CCAGTCTCCA rGlnSerPro	TCCTCACTGT	450
CTGCATCTGT	AGGAGACAGA	GTCACCATCA	CTTGTCGGGC	GAGTCAGGGT	500
ATTAGCAGCT	GGTTAGCCTG	GTATCAGCAG		AAGCCCCTAA	550
GTCCCTGATC	TATGCTGCAT	CCAGTTTGCA	LysProGluL AAGTGGGGTC	CCATCAAGGT	600
TCAGCGGCAG	TGGATCTGGG	ACAGATTTCA	nSerGlyVal CTCTCACCAT	CAGCAGCCTG	650
CAGCCTGAAG	ATTTTGCAAC	TTATTACTGC	hrLeuThrIl CAACAGTATA	ATAGTTACCC	700
GlnProGluA ACCCACAGTG	spPheAlaTh TTACACACCC	rTyrTyrCys AAACATAAAC	GlnGlnTyrA CCCCAGGGAA	GCAGATGTGT	750
o GAGGCTGGGC	TGCCCCAGCT	GCTTCTCCTG	ATGCCTCCAT	CAGCTGAGAG	800
TGTTCCTCAG	ATGCAGCCAC	ACTCTGATGG	TGTTGGTAGA	TGGGGAC	847







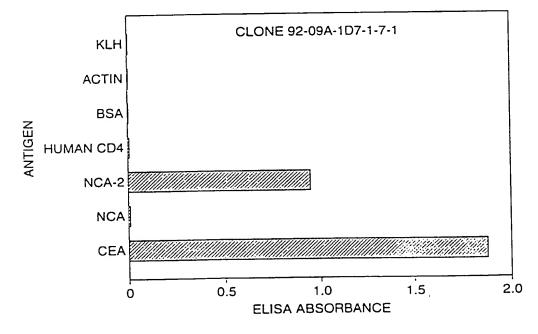
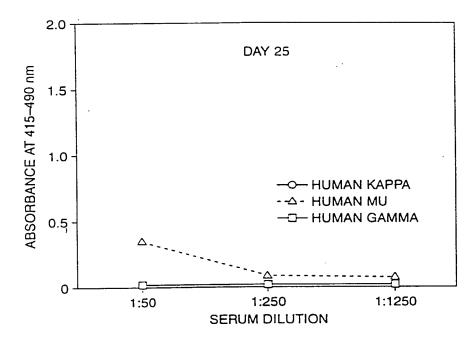


FIG. 46

		48/89)
MOUSE Cy	CCAAAACGACACCCCATCTGTCTATCCACT CCAAAACGACACCCCATCTGTCTATCCACT	CCAAAACAACACCCCATCAGTCTATCCACT CCAAAACAACACCCCATCAGTCTATCCACT CCAAAACAACACCCCATCAGTCTATCCACT CCAAAACAACACCCCATCAGTCTATCCACT	CTACAACAGCCCCATCTGTCTATCCTT CTACAACAACAGCCCATCTGTCTATCCTT CTACAACAACAGCCCATCTGTCTATCCTT
•	(GGT.91G0ACGTCTGGGGCCAAGGACACGGTCACCGTCTCCTCAG CCAAAACGACACCCCCATCTGTCTATCCACT GCTcTTGA191CTGGGGCCAAGGGACAA1GCTCACCGTCTTCAG CCAAAACGACACCCCCATCTGTCTATCCACT	GCTTTTGATATCTGGGGCCAAGGACAATGGTCACCGTCTTCAG CCAAACACACCCCCATGGTCTATCACT GCTTTAGATATCTGGGGCCAAGGACAATGGTCACCGTCTTCAG CCAAACACACCCCCATCAGTCTATCACT c	GATATCIGGGGCCAAGGACAATGGTCACCGTCTCTTCAG CTACAACAGCGCCCATCTGTCTATCCCTT TTGACTATTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG CTACAACAACGGCCCATCTGTCTATCCCTT GCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTTCAG CTACAACAACACCCCATCTGTCTATCCCTT TACTACTACTACGATGGACGTCTGGGGCCAAGGGACCACGTCGTCCTCTCTCT
HUMAN n D n	cattTATGGTTCGGGAGTTAcg cACTGGGcattggat	ACTGGGAtgat cagagagagat catagagACTATatTTCGGGGAGTTATTttcc ACTGGGAtgat	catgggtctatg gagagcggtcACTGGGAtcg aggGACCCCctgat caGGGCCT
VAZS1	DXP'1 J6 G1 GCCTCGGACACCGCCATGTATTACTGTG+GAGA DHQS2 J3 G1 GCCTCGGACACCGCCATGTATTACTGTGCGAGA	2 DHOSZ J3 G2b GCCTCGGACACCGCCATGTATTACTGTGCGAGA 3 D? J3 G2b GactcgGaCACCGCCATGTATTACTGTGCGAGA 4 DXP'1 J4 G2b GCCTCGGACACCGCCATGTATTATGTGEGGA 10 DHOSZ J3 G2b GCCTCGGACCGCCATGTATTACTGTGCGAGA	GCCTCGGACACCGCATGTATTACTGTGCGAGA GCCTCGGACACCGCATGTATTACTGTGCGAGA GCCTCGGACACCGCCATGTATTACTGTGCGAGA GCCTCGGACACCGCCATGTATACTGTGCGAGA
	5 DXP'1 36 G1 7 DHQS2 33 G1	2 DHQS2 J3 G2b 3 D? J3 G2b 4 DXP'1 J4 G2b 10 DHQS2 J3 G2b	1 D? 33 G3 6 DH052 34 G3 8 DIR2 33 G3 9 DIR2 15 G3





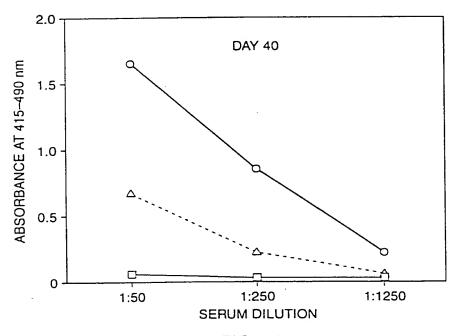


FIG. 48



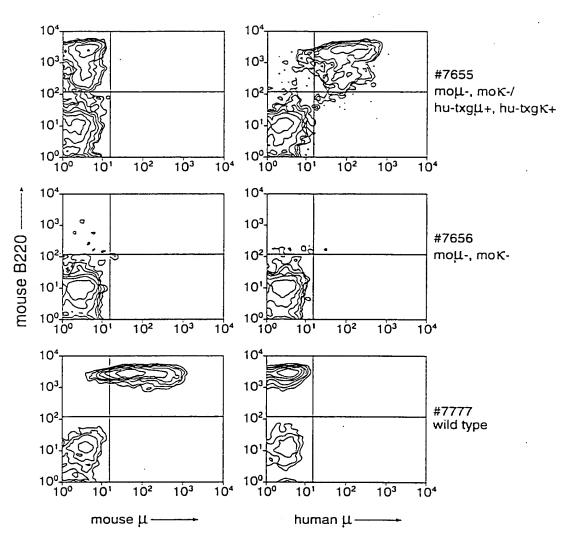


FIG. 49

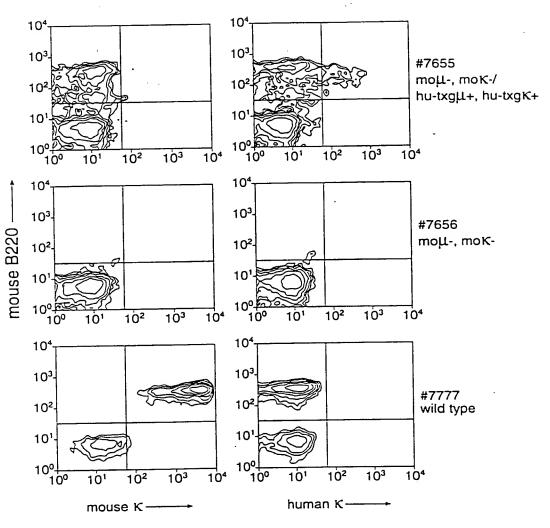


FIG. 50

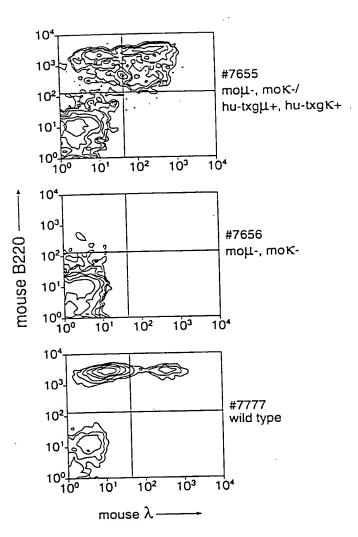


FIG. 51

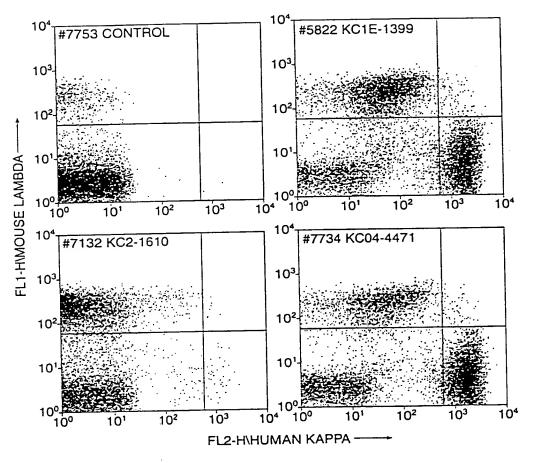
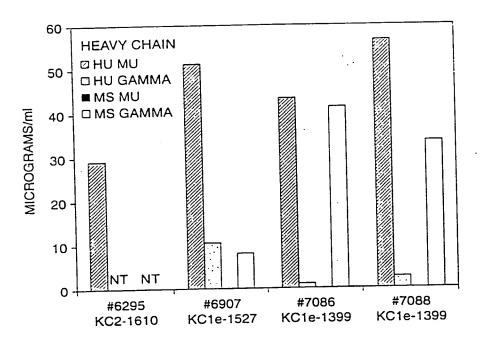


FIG. 52





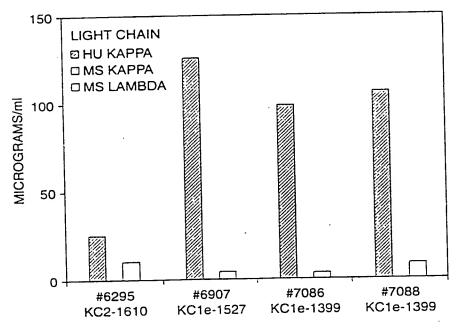


FIG. 53



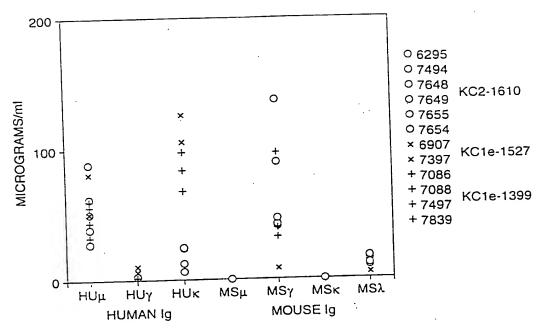


FIG. 54

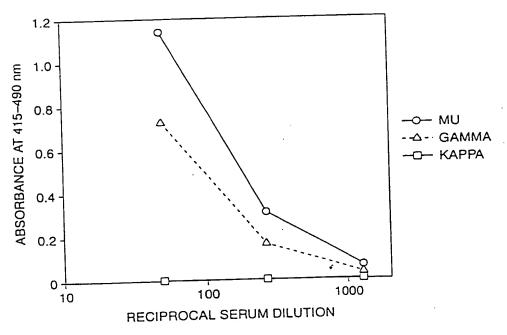
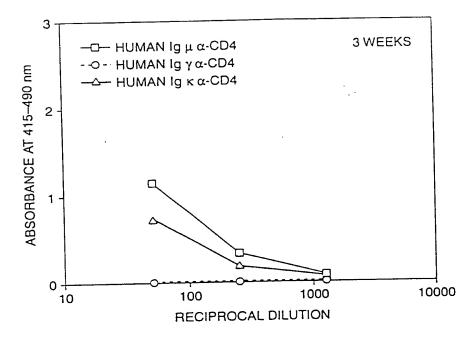


FIG. 55





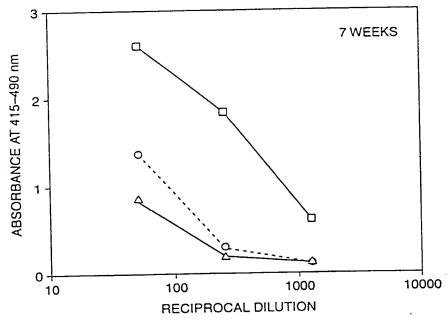
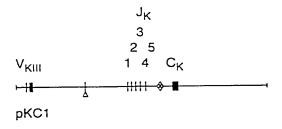


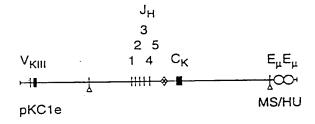
FIG. 56

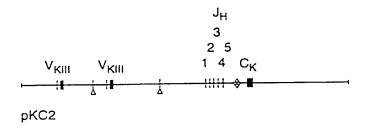




LIGHT CHAIN MINILOCI







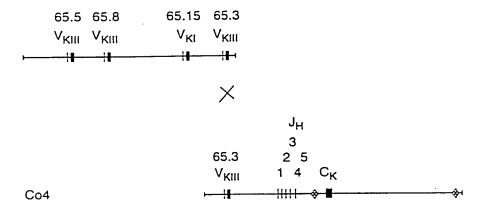


FIG. 57A

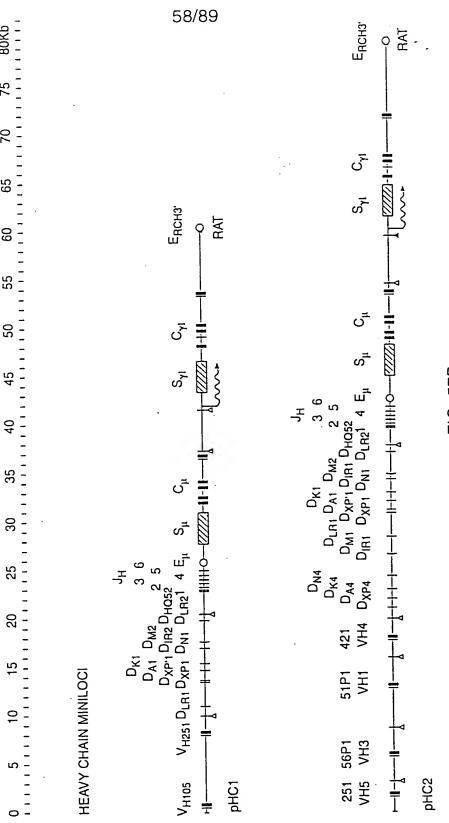


FIG. 57B

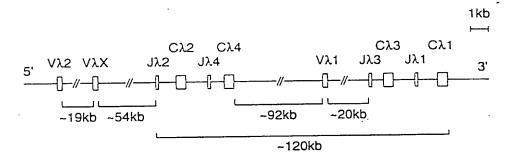
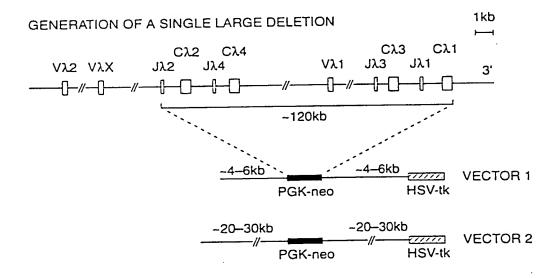


FIG. 58



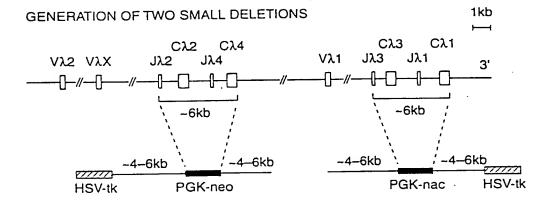
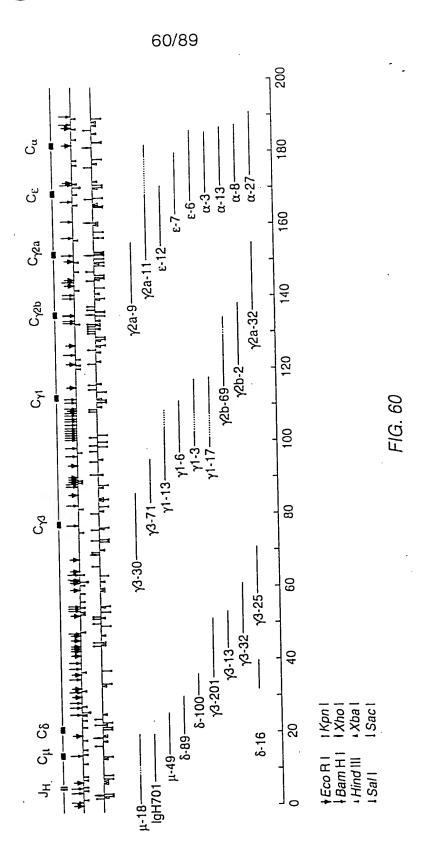


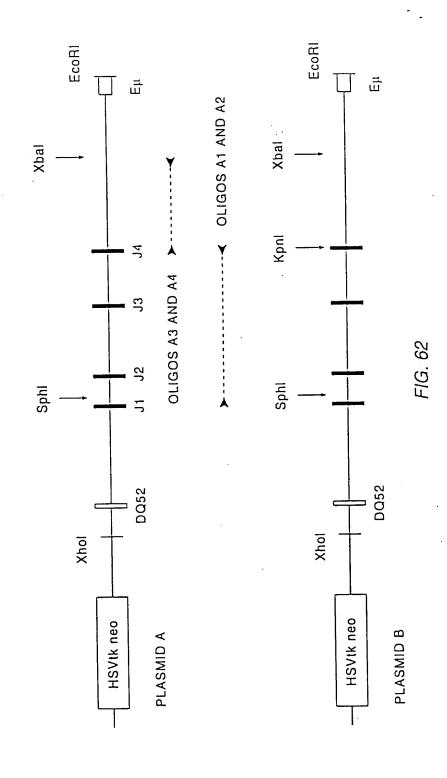
FIG. 59



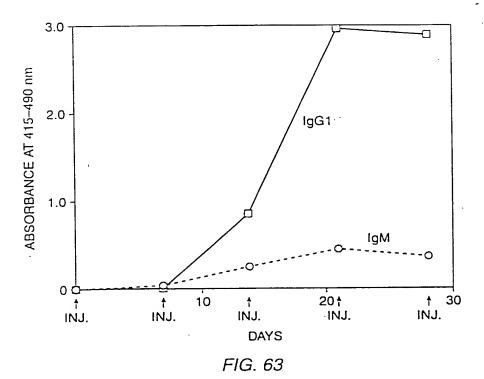


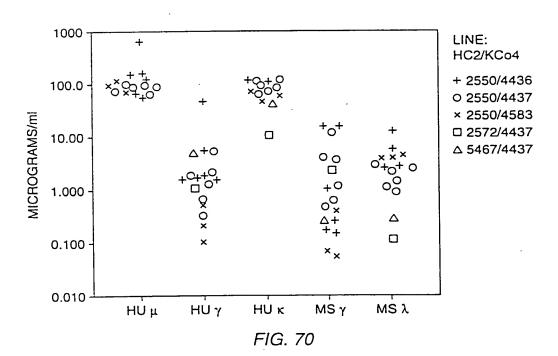
CGAGAGGGGGGGGGGAAGACTACTATCCCAGGCAGGTTTTAGGTTCCAGAGTCTGCGAG AAATCCCACCATCTACCCACTGACACTCCCACCAGTCCTGTGCAGTGATCCCGTGATAAT CGGCTGCCTGATTCACGATTACTTCCCTTTCGGCACGATGAATGTGACCTGGGGAAAGAG TGGGAAGGATATAACCACCGTGAACTTTCCACCTGCCCTCGCCTCTGGGGGACGGTACAC CATGAGCAGCCAGTTAACCCTGCCAGCTGTCGAGTGCCCAGAAGGAGAGTCCGTGAAATG TTCCGTGCAACATGACTCTAACCCCGTCCAAGAATTGGATGTGAATTGCTCTGGTAAAGA ACGTTAGGGGGTCAGCTAGGGGTGGGATAAGTCCTACCTTATCTAGATCCATATATCCCT CTGATGCACACCCTCACAGGAATCCCTCAGAAACCTCCACTATGGGGGATTGGGGGAAGGA AGCGTAAACAGGTCTAGAAGGAGCTGGAGGCCTCAGAACATCCAGAAACGGGGACAGCAA AGGAGACAAGGAGAATATACTGATTTGCTAGGACATCTTCTGTTACAGGTCCTACTCCTC CTCCTCCTATTACTATTCCTTCCTGCCAGCCCAGCCTGTCACTGCAGCGGCCAGCTCTTG AGGACCTGCTCCTGGGTTCAGATGCCAGCATCACATGTACTCTGAATGGCCTGAGAAATC CTGAGGGAGCTGCTTTCACCTGGGAGCCCTCCACTGGGAAGGATGCAGTGCAGAAGAAAG GCTGGAACAGTGGCGCATCATTCAAGTGCACAGTTACCCATCCTGAGTCTGGCACCTTAA CTGGCACAATTGCCAAAGTCACAGGTGAGCTCAGATGCATACCAGGACATTGTATGACGT CTTATATCACAGAGGGAAATTGGAGCTATCTGAGGAACTGCCCAGAAGGGAAGGCAGAG GGGTCTTGCTCCTTGTCTGAGCCATAACTCTTCTTTCTACCTTCCAGTGAACACCTTC CCACCCAGGTCCACCTGCTACCGCCGCCGTCGGAGGAGCTGGCCCTGAATGAGCTCTTG TCCCTGACATGCCTGGTGCGAGCTTTCAACCCTAAAGAAGTGCTGGTGCGATGGCTGCAT GGAAATGAGGAGCTGTCCCCAGAAAGCTACCTAGTGTTTGAGCCCCTAAAGGAGCCAGGC GAGGGAGCCACCACCTACCTGGTGACAAGCGTGTTGCGTGTATCAGCTGAAACCTGGAAA CAGGGTGACCAGTACTCCTGCATGGTGGGCCACGAGGCCTTGCCCATGAACTTCACCCAG AAGACCATCGACCGTCTGTCGGGTAAACCCACCAATGTCAGCGTGTCTGTGATCATGTCA GAGGGAGATGGCATCTGCTACTGAGCCACCCTGCCTGTCCCTACTCCTAGAATAAACTCT GTGCTCATCCAAAGTATCCCTGCACTTCCACCCAGTGCCTGTCCACCACCCTGGGGTCTA CGAAACACAGGGAGGGGTCAGGGCCCAGGGAGGGAGAAATACCACCACCTAAGC

FIG. 61









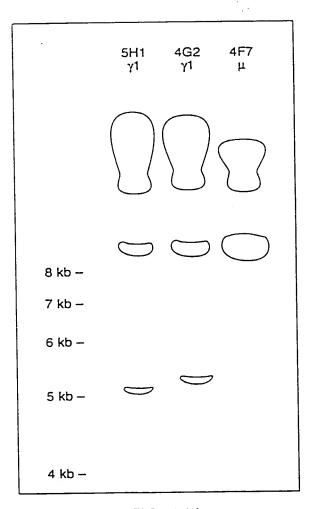
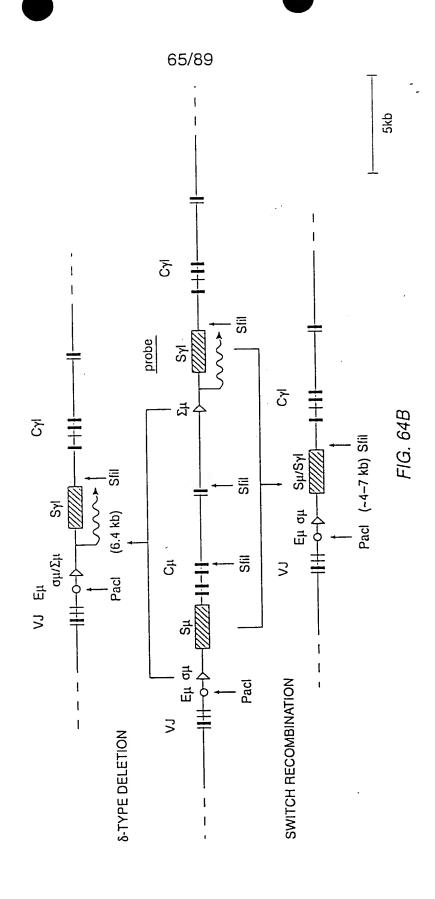


FIG. 64A



DOVELT ESCO

66/89 2357.t4 DXP'1 J4 gcctcggacaccgccatgtattaTtgtgTgaga CATAGGGactatATttcggggagttattTTCC tgactactggggccagggaacccttggtcaccgtctcctcag ccaaaacaacacccccatcagtctatccac gcttttgatatctggggccaagggacaatggtcaccgtctcttcag ccaaaacaacacccccatcagtctatccac gctíttgatútctggggccaagggacaatgítcaccgtctcttcag ccaaaacgacacccccatctgtctatccac gcttttgatatctggggccaagggacaatggtcaccgtctcttcag ccaaaacaacacccccatcagtctatccac gctttagatatctggggccaagggacaatggtcaccgtctcttcag ccaaaacaacacccccatcagtctatccac gatatciggggccaagggacaaiggicaccgiciticag ciacaacaacagccccaicigiciaicci tttgactaTtggggccagggaaccctggtcaccgtctcctcag ctacaacaacagccccatctgtctatccct gcttttgatatctggggccaagggacaatggtcaccgtctcttcag ctacaacaacagccccatctgtctatccct tactactactacggtatggacgtctggggccaagggaccacggtcaccgtctcctcag ctacaacaacagccccatctgtctatccct cggtGtgAacgtctggggccaagggaccacggtcaccgtctcctcag ccaaaacgacacccccatctgtctatccac mouse y2b mouse γ3 mouse γ1 ح 2357.t5 DXP'1 J6 gcctcggacaccgccatgtattactgtgĪgaga CATTtatggttcggggagttaCG 2357.t6 DHQ52 J4 gcctcggacaccgccatgtattactgtgcgaga GAGAGCGGTCactggggaTCG N O N 2357.t7 DNOS2 J3 gcctcggacaccgccatgtattactgtgcgaga CactgggCATTGGAT 2357.t8 DIR2 J3 gcctcggacaccgccatgtattactgtgcgaga AGGgaccccCTGAT 2357.t1 D? J3 gcctcggacaccgccatgtattactgtgcgaga CATGGGTCTATG 2357.t3 D? J3 gActcggacaccgccatgtattactgtgcgaga CAGGGAGAGAT 2357.t2 DHQS2 J3 gcctcggacaccgccatgtattactgtgcgaga actggggaTGAT 2357.t10 DHQS2 J3 gcctcggacaccgccatgtattactgtgcgaga actggggaTGAT 2357.t9 DIR2R J6 gcctcggacaccgccatgtattactgtgcgaga CGggggcct V₁₁251

FIG. 65

human





SØ SZ a S3 ATCATCTATCTGGTGACTCTGATACCAGATACAGCCCGTCCTTCCAAGGCCAGGTC							COR II
20 S2 o S3 60 VIPSS1.GL TCTCTGAAGATCTCCTGTAAGGTTCTGGATACAGCTACTGGATGGCTGGGTGCGCGGAAAGGCCTGGAGTGGATGGGATGTGTTCTGTGTGATACCAGATACGAGTCCTTCCAAGGCCAGGTC J2	7.599.7	J3 2599.25 14	8, 262.5	2599.23 2599.24	2599.28 16	Z599.10	COR I

FIG. 66A.

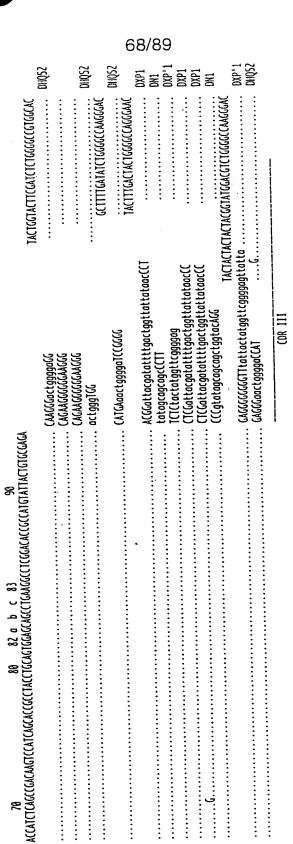


FIG. 66A.2

10 10 10 10 10 10 10 10			69/89	
CTGAAGATCTCCTGTAAGGGTTCTGGATAKAGCTT A T T T T T T T T	30 TACCAGCTACTGGATGGGTGGGGGGGGGGGGGGAAAGGCCTGGAGTGGATGGGATGGGATCATCTATCCTGGTGATTGTAGATGGATACAGGCCGTCCTTCCAAGGCCAGGTC	(0)		
91251.GL TCT J2	20 GL TCTCTGAAGATCTCCTGTAAGGGTTCTGGATACAGCTTTA	. Sp28		

FIG. 66B.1

				-	70/8	39				
	ZSÒHO	7S)III		011052	011052	OXP'1		OXP.1		
AACTGGTACTTCGATCTCTGGGGCCGTGGCACCCTGGTC	GCTTTGATATCTGGGGCCAAGGGACAATGGTC	TACTTTGACTACTGGGGCCAGGGAACCCTGGTC		c		૽ૡ)¥	DOCATI. TACTACGGTATGGACGTCTGGGGCCAAGGGACCACGTC		
		GTAaactgggATCGG	CATAAGGCGGGATCAAC CATAAGGCGGGGATCAAC	CATAAGGGGGGATCAAC	CATAAGGGGGATCAAG	CATAAGGGGGGATCAAC CATAAGAGGGGGGATCAAC	CATAAGGCGGGATCAAC	CAGGgtattactatggttcggCAaAttattat TACTACTA	נננננפפנפ	COR 111
70 ACCATCTCAGCCGACAAGTCCATCAGCACCGCTACCTGCAGCAGCCTGAAGGCCTCGGACACCGCCATGTATTACTGTGCGAG	CAGGactggggaTCGGGAA		T CATARGEGGGGATCAAC T CATARGEGGGGGATCAAC	T CATAMOGUGOGATCAMC	1	T (ATAMOGOGOGATCAAC	T CATAGGGGGGTGAAC	CAGGGtattactatggttaggAaktattataacATTA	Α	

FIG. 66B.2

71/89	
29. 14 TCTCOMAGNETCTGATACGATTCGATACGATCGATCGATCGATCGATCGA	F/G. 67A





MASS. G 28 38 52 53 56 53 56 53 56 53 55 55	SØ S2 o S3 GGATGGGGATCATCTTGGTGATGTTGATACAGATACAGCCGTCCTTCCAAGGCCAGGTC	6	9 T 1 1) 1 y 9	CDR 11
28 GAICTCTGTAAGGCTTCTGGATACAGCTTTACCAGCTACTGGA C	40 TCGCTGGGTGCGCCAGATGCCCGGGAAAGGCCTGGAGTG					, A	-
	20 SATCTCCTGTAAGGGTTCTGGATACAGCTTTACCAGCTACTGGAT	J	: : :			, T C C C A	CORT

IG. 67B.1

		25 _1	27.72		JM2 r	73/			. .		
			OXP'1 DHQS2		ON1/OM2r	N I	OXP'1			-	
TACTGGTACTTCGATCTCTGGGGCCGTGGCACCCTGGTC	GCTTTGATATCTGGGGCCAAGGGACAATGGTC	TACTTTGACTACTGGGGCGAGGAACCCTGGTC	GGgtattaTtatgAttcggggaCttattataaGTCTACCCA	ΑΑ);	•	A	AACTGGTTCGACCCTGGGGCCAGGAACCCTGGTC	adtat IACTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTC		
		(ATTGGctoaktggggaT (GGGattacgatatttgactggttattatGCG	GGgtattaTtatgAttcggggaCttattataaGT ctaactggCT CAITT	CAICTT	CAAACT CATggtatagcagcagctggtacgtggttcGACC CACGC	. CATCTT . CATCTT GCCgggtataCcagcagctggtT	CATCTT GegettcggggaTttattatT CAAACCC		. CTCCCCATGACAGT . CGGGGtactatggttcggggggttattat TACTACTAC	CATGOGCOGCLOGLOCAGGT GATATGGGGGGGCCTC C	
80 82 a b c 83 accatctcagcggalaagtccatcagcacgctagctggaagggaag	.CGCAGGGGGGATA	. CATIGOCtoaktggggaT					(6	. G GGATCGTGG	. GTCCCAATGACAGT . CTCCCAATGACAGT . CGGGGtactatggttcqttat IACTACT	D) CO	

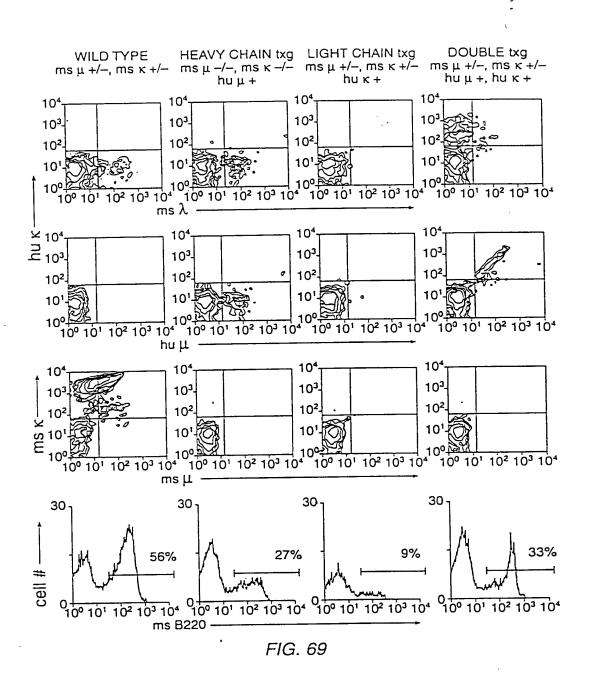
FIG. 67B.2

	74/89	CCAGGGCAGAGTC	
Minor Lut. Literana Control Co		TEGGTGAAGGTETECTGCAAGGETTETGGAGGCAECTTEAGCTATGETATGGTGEGGGGGGGCAAGGCEETGGAAGGGETTGAGTGGAAGGATCATECETATG AECETGTECETCACCTGCGGTGTTATGGTGGGGGCCTTCAGTGGTTACTGGAGCTGGATCCGCCAGCCCCGGGGAAGGGGCTGGATTGGGGAATCAATC	

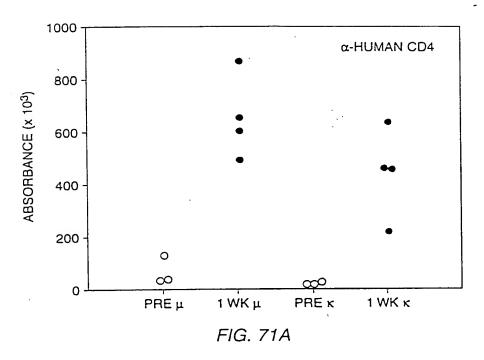
TACTGGTACTTCGATCTCTGGGGCCGTGGCCTGGTC T T CT T T T T T	T T ACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTC	DK1 DK1 DXP DXP DXP	GCTTTGATATCTGGGGCCAGGGACAATGGTC ONQS2 TACTTTGACTACTGGGGCCAGGGAACCCTGGTC	5GAC DR 111 -
70 ACCATCTCCAGAGACAATTCCAAGACGCTGTATTCTGTGTATTACTGTGCAGA ACCATCTCCAGAGACTGCAAATGAACAGCCTGAGAGCTGAGACTGGCTGTGTATTACTGTGCGAGA T G GAGTCTTCCGG T G AGGTCTTCCGG T G GAGTCTTCCGG T G GAGTCTTCCGG T G GAGTCTTCCGG T GAGTCTTCCGG T GAGTCTTCCGG T GAGTCTTCCGG T GAGTCTTCCGG T GAGTCTTCCGG	· · · · · · · · · · · · · · · · · · ·	GATCAGGGGGGGtatagtggctacgGGTGGGG GATCAGGCGCGtatagtggctacgGGTGGGG CattactatggttcggggggttatAG CattactatggttcggggggttatAG GatGagactacG	ACGATTACCGCGGGAAATCCACGAGCATAGCTAGCTAGCT	GAACTTATTT GGAGCTGOCCEGG GGCAGCTGOCCEGG AGAGAGTGAGGGAE GOR I

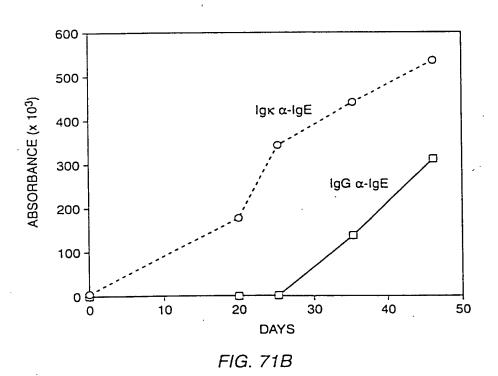
FIG. 68B

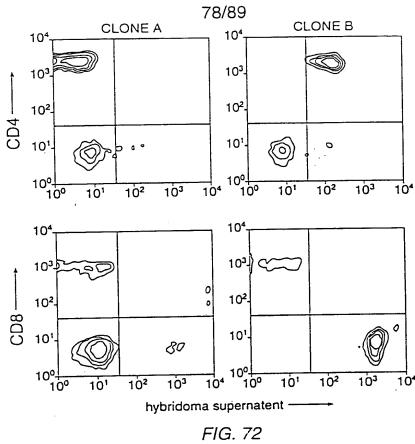












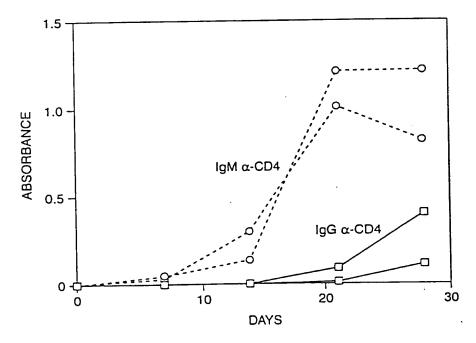


FIG. 73



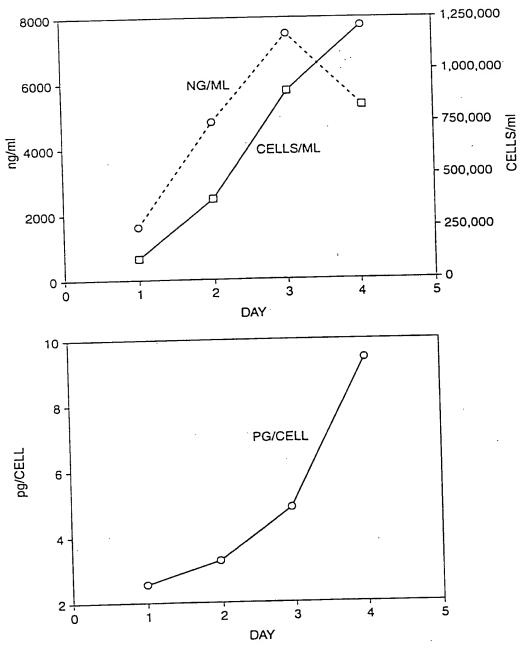


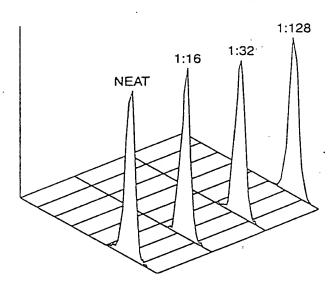
FIG. 74





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RPA-T4/2C11-8 #12:BDPHARMCOMP004\FL2-H\FL2-HEIGHT



Leu-3a/2C11-8 #12:BDPHARMCOMP025\FL2-H\FL2-HEIGHT

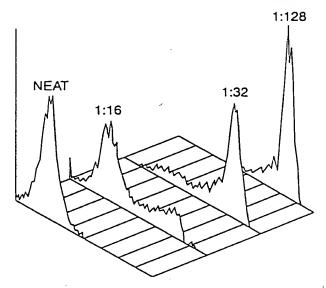


FIG. 75

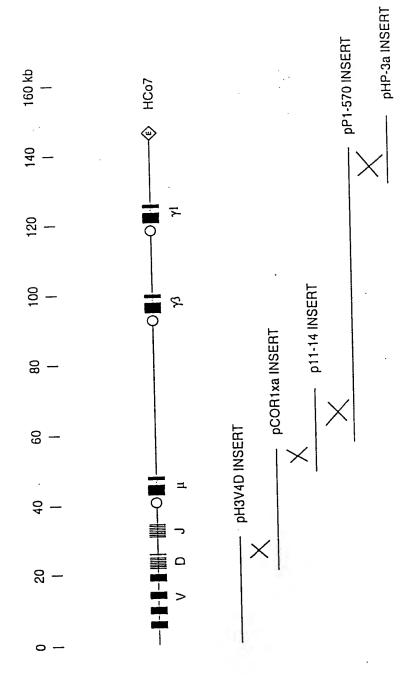


FIG. 76





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pGP2b sequence:

AAAAAAGCCCGCTCATTAGGCGGGCTCTTGGCAGAACATATCCATCGCGTCCGCCATCTCCAGCAGCCGCACGCGGCGCA TCTCGGGCAGCGTTGGGTCCTGGCCACGGGTGCGCATGATCGTGCTCCTGTCGTTGAGGACCCGGCTAGGCTGGCGGGGT AGCAACAACATGAATGGTCTTCGGTTTTCGTAAAGTCTGGAAACGCGGAAGTCAGCGCCCTGCACCATTATGTTGAGTGATTTTTCTCTGGTCCCGCCGCATCCATACCGCCAGTTGTTTACCCTCACAACGTTCCAGTAACCGGGCATGTTC ATCATCAGTAACCCGTATCGTGAGCATCCTCTCTCGTTTCATCGGTATCATTACCCCCCATGAACAGAAATTCCCCCTTAC ACGGAGGCATCAAGTGACCAAACAGGAAAAAAACCGCCCTTAACATGGCCCGCTTTATCAGAAGCCAGACATTAACGCTTCGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGA TGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTC ${\tt TCAGTGGAACGAAAACTCACGTTAAGGGATTTTCGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATT}$ <u>AAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCA</u> CCTATCTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGG AGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTGCAGGCATCGTGGTGTCACGCTCGTCGTT TGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTA TCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTAT TTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCA CCCAACTGATCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAA CGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATT GTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTG AG

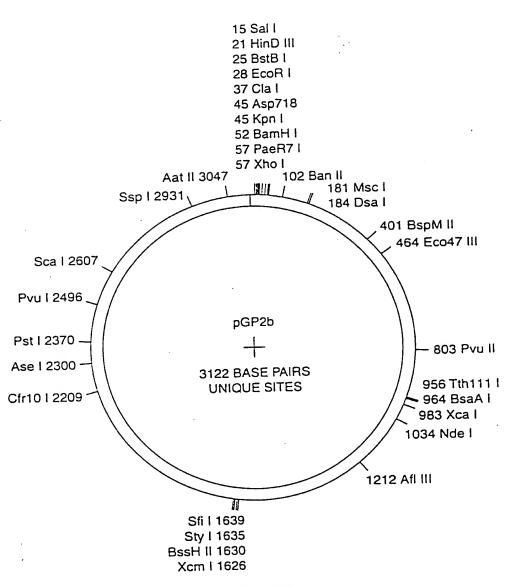
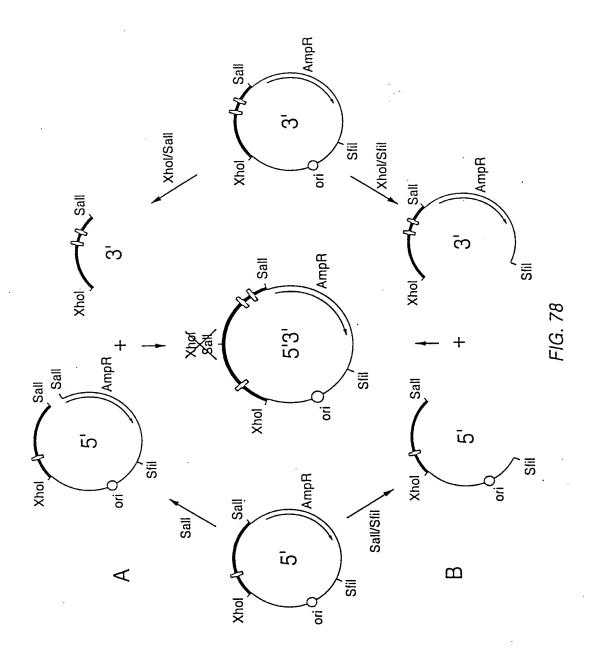


FIG. 77B



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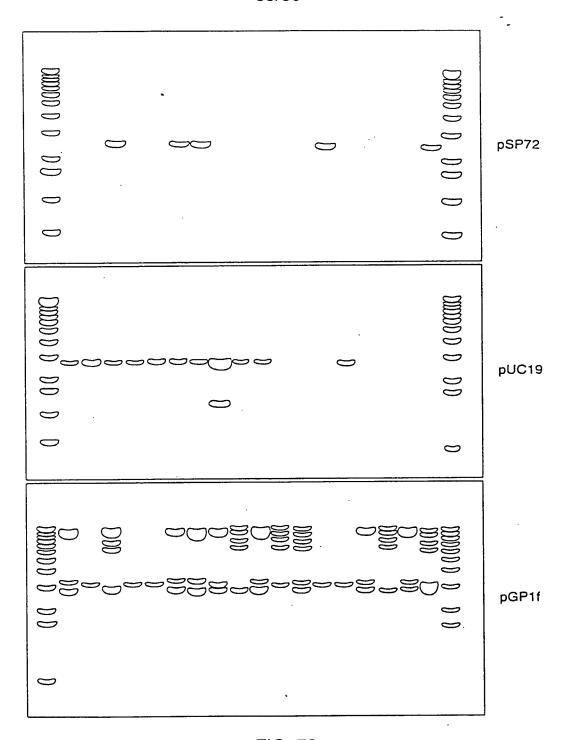
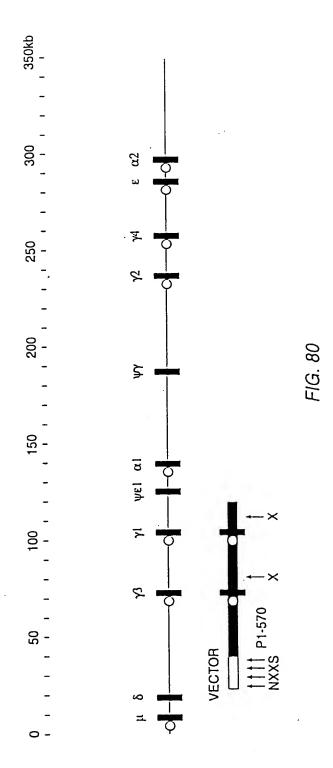
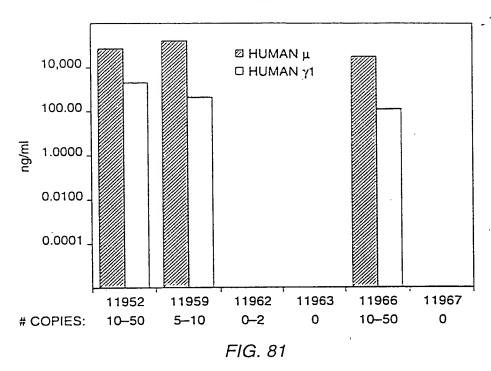
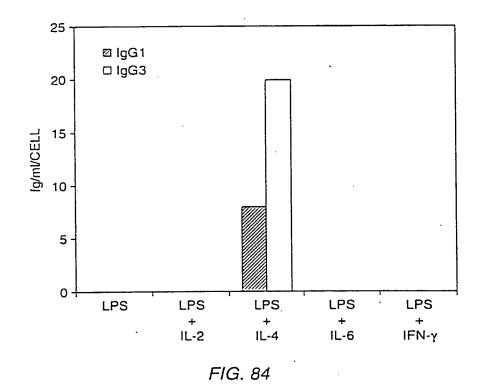


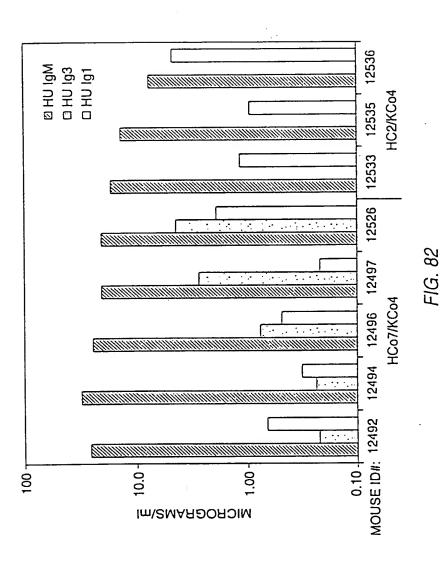
FIG. 79



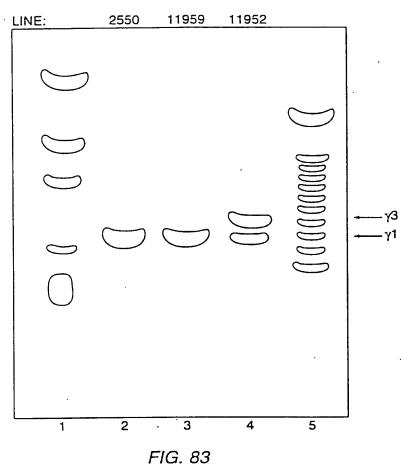












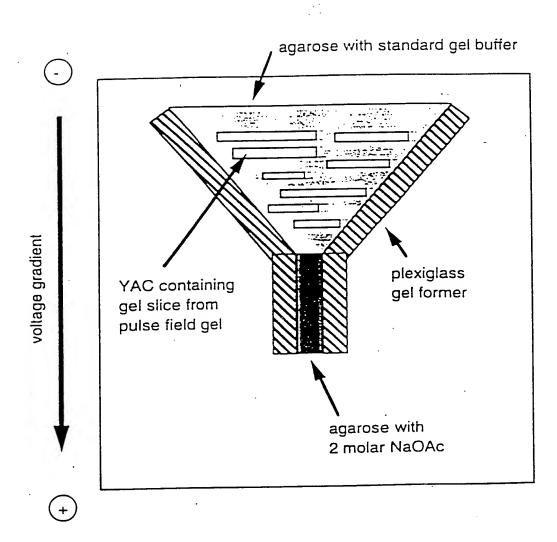


Figure 85

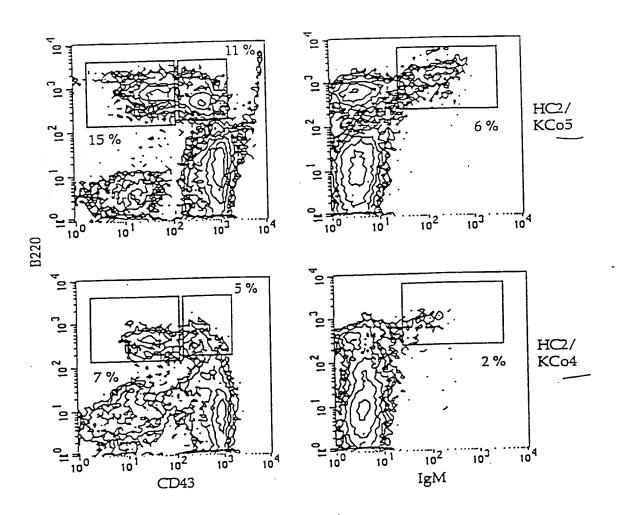


Figure 86

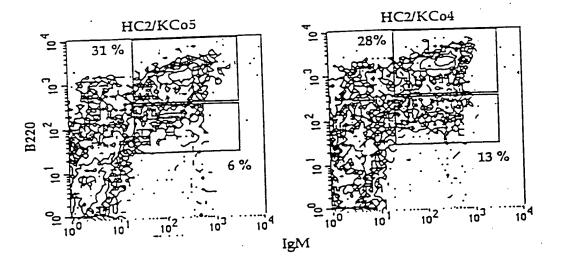


Figure 87

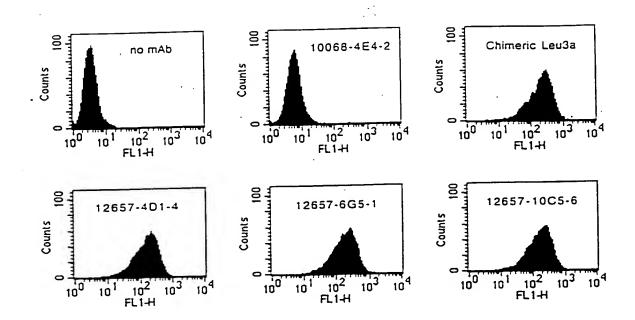


Figure 88

Cells pre-incubated with:

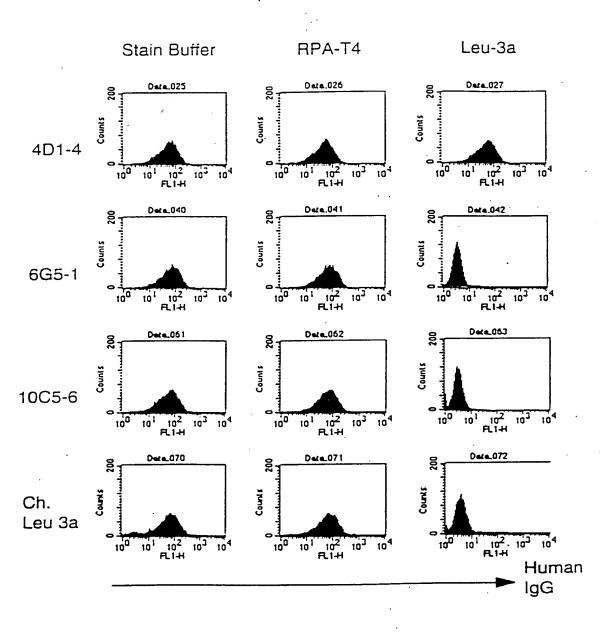


Figure 89

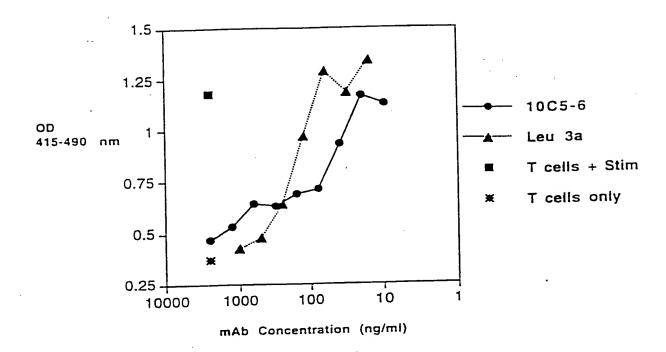


Figure 90

Figure 91

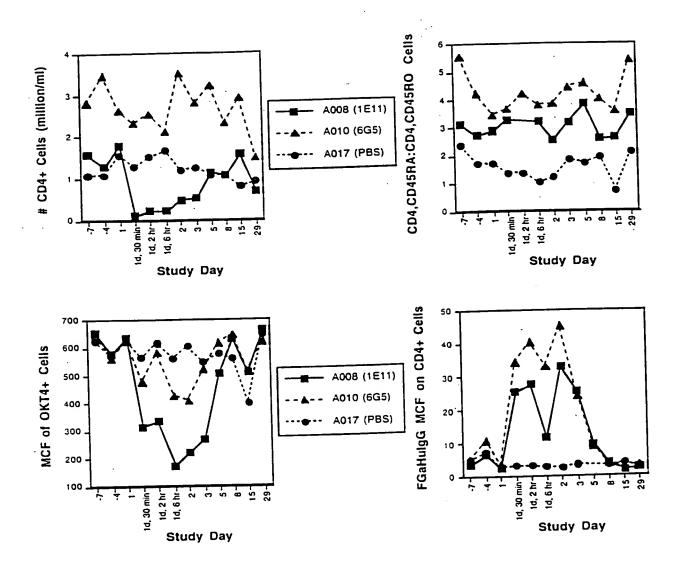


Figure 92

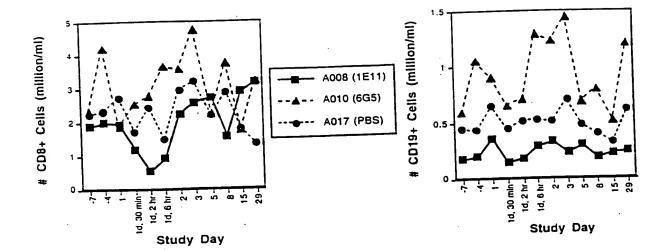


Figure 93

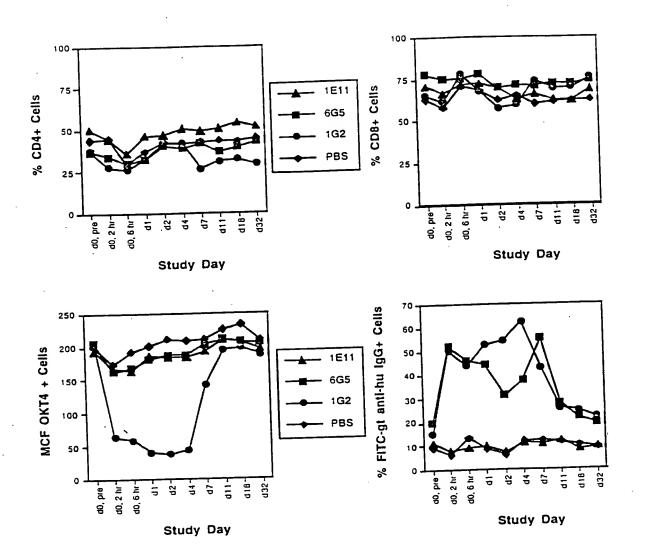


Figure 94

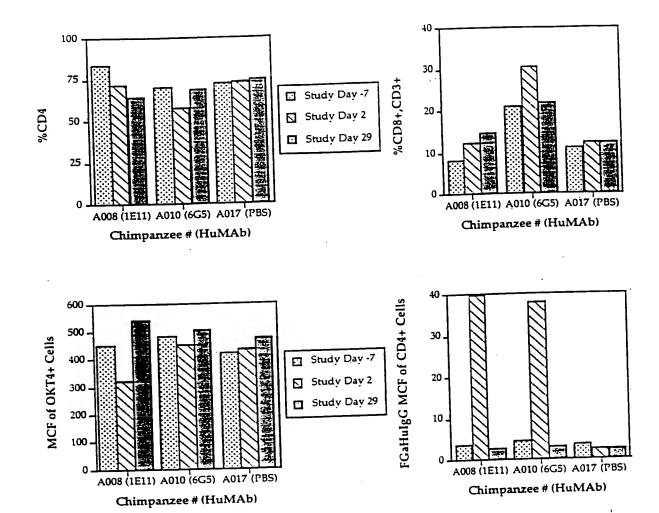


Figure 95

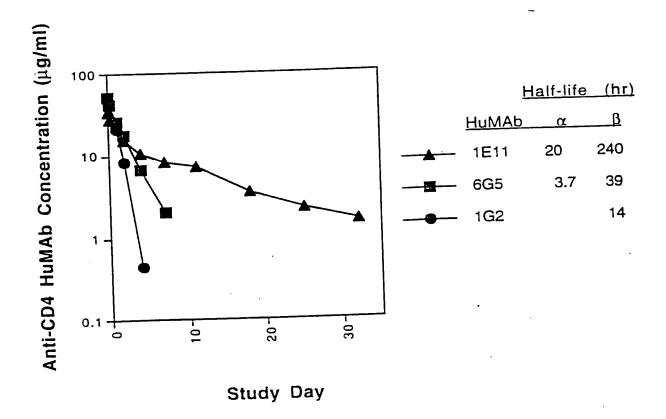
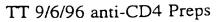
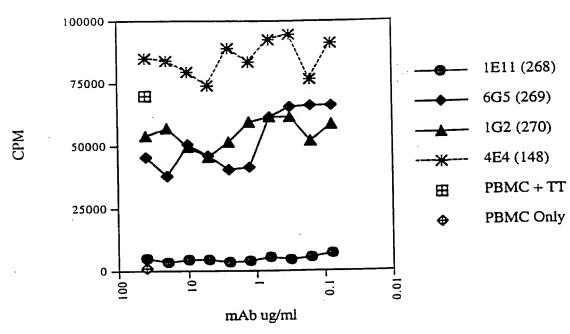


Figure 96





TT 10/2/96 anti-CD4 Preps

